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<p>(54) Title: REAGENTS AND METHODS FOR DETECTING GENES RELATED TO MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH AS CHICKEN</p>		
<p>(54) Titre: REACTIFS ET METHODES POUR LA DETECTION DE GENES LIES AU COMPLEXE MAJEUR D'HISTOCOMPATIBILITE D'OISEAUX D'ELEVAGE, TELS QUE LE POULET</p>		
<p>(57) Abstract</p>		
<p>The invention concerns nucleic acid molecules for detecting the MHC genes involved in phenomena of resistance or proneness to the development of virus-induced tumours. The primers prepared from said molecules can be used in a method for genotyping domestic fowl, characterised in that it consists in: amplifying a nucleic acid sample derived from the animal under study using one or several pairs of primers capable of being specifically hybridised with the nucleic acid of a pleomorphic region of the Rfp-Y or B systems of the MHC of said fowl; detecting the resulting PCR products.</p>		
<p>(57) Abrégé</p>		
<p>L'invention vise des molécules d'acides nucléiques permettant de détecter ceux des gènes du CMH impliqués dans les phénomènes de résistance ou de susceptibilité au développement de tumeurs viro-induites. Les amorces élaborées à partir de ces molécules sont utilisables dans une méthode de génotypage d'oiseaux d'élevage et notamment du poulet, caractérisée en ce qu'elle comprend : l'amplification d'un échantillon d'acide nucléique provenant de l'animal à étudier à l'aide d'un ou de plusieurs couples d'amorces capables de s'hybrider spécifiquement avec l'acide nucléique d'une région polymorphe des systèmes Rfp-Y ou B du CMH desdits oiseaux et la détection des produits de PCR obtenus.</p>		

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REACTIFS ET METHODES POUR LA DETECTION DE GENES
LIES AU COMPLEXE MAJEUR D'HISTOCOMPATIBILITE D'OISEAUX
D'ELEVAGE, TELS QUE LE POULET

5 L'invention a pour objet la détection de gènes
liés au complexe majeur d'histocompatibilité (CMH)
d'oiseaux d'élevage, tels que le poulet. A ce titre, elle
concerne des molécules d'acides nucléiques permettant de
détecter ceux des gènes du CMH impliqués dans les
10 phénomènes de résistance ou de susceptibilité au
développement de tumeurs viro-induites. L'invention
concerne également les applications de ces molécules
d'acides nucléiques, notamment pour le développement de
tests de génotypage chez les oiseaux d'élevage, en
15 particulier le poulet, et pour la sélection d'animaux
d'intérêt.

Les maladies virales infectieuses sont
redoutées des éleveurs en raison de leur caractère
20 contagieux qui conduit à des pertes importantes
d'animaux.

La vaccination a constitué une prophylaxie
efficace jusqu'à l'émergence de souches hypervirulentes,
25 rendant nécessaire l'identification des haplotypes
résistants.

Diverses méthodes ont ainsi été proposées pour
tenter de sélectionner ceux des animaux qui sont capables
30 de résister à de telles pathologies et ceux qui sont au
contraire susceptibles d'être affectés.

Les techniques les plus utilisées en routine
sont basées sur des polymorphismes sérologiques ou de

type RFLP. Toutefois, ces méthodes ne fournissent pas de connaissances précises sur le phénomène de résistance ou de susceptibilité à la maladie, en particulier par manque de caractère discriminant vis-à-vis des gènes des systèmes B ou Rfp-Y du CMH.

Les travaux des inventeurs sur le séquençage de gènes du CMH a montré la complexité génétique de cette région, ce qui les a conduits à prendre en compte un autre type de polymorphisme, à savoir basé sur la séquence de ces gènes et des régions apparentées, telles que celles de leurs promoteurs et des régions microsatellitaires. Les inventeurs ont ainsi mis au point des moyens pour disposer de molécules oligonucléotidiques hautement spécifiques des polymorphismes observés, permettant d'identifier les parties de gènes, et même les sites impliqués dans le contrôle de la résistance ou de la susceptibilité au développement de tumeurs.

Le caractère spécifique de ces molécules, vis-à-vis d'un gène donné de l'un des systèmes du CMH, en fait des outils discriminants particulièrement fiables pour identifier avec précision la capacité de résistance ou de susceptibilité du poulet étudié, ou d'autres oiseaux, à une infection virale, et pour étudier au niveau moléculaire les séquences du CMH impliquées.

L'invention a donc pour but de fournir des molécules d'acides nucléiques permettant de détecter spécifiquement, chez les oiseaux d'élevage et en particulier chez le poulet, les gènes liés au CMH impliqués dans les phénomènes de résistance ou de susceptibilité au développement de tumeurs viro-induites.

Elle vise également à fournir une méthode et un kit de détection de génotypes de mise en oeuvre aisée en routine.

5 Les molécules d'acides nucléiques de l'invention sont caractérisées en ce qu'il s'agit de molécules, isolées de leur environnement naturel, d'acides nucléiques de gènes codant pour des protéines impliquées dans le contrôle de la résistance ou de la
10 susceptibilité au développement de tumeurs viro-induites chez les oiseaux d'élevage, telles que celles de la maladie de Marek chez le poulet, avec le cas échéant, les régions qui leur sont attachées, telles que celles du promoteur ou microsateellites. Le terme gène tel
15 qu'utilisé dans la description et les revendications englobe ces régions.

Ces molécules d'acides nucléiques sont plus spécialement caractérisées en ce qu'elles présentent les
20 séquences d'acides nucléiques de gènes du système B ou du système Rfp-Y du CMH des oiseaux d'élevage, à l'exception des séquences des gènes de classe II B-L, du gène 17.5, du gène 12.3 et du gène B-FIV de classe I, ou sont capables de s'apparier avec l'un des brins d'un gène
25 capable de coder pour une protéine telle que définie ci-dessus dans des conditions faiblement stringentes.

L'appariement dans des conditions de faible stringence auquel il est fait référence ci-dessus est
30 réalisé à température ambiante, dans un milieu 0,1 SSC, avec lavage à température ambiante.

Les gènes de classe II B-L sont décrits dans Immunogenetics 31:179-187, 1990 et Eur. J. Immunol, 1993, 23:1139-1145.

5 Le gène 17.5 appartient à la superfamille des gènes codant pour les lectines et le gène 12.3 à la famille des gènes codant pour des protéines liant la guanine (guanine nucleotide-binding protein). Ce gène est décrit dans Immunogenetics 39:221-229, 1994.

10 Le gène 12.3 est décrit dans P.N.A.S. USA, vol. 86, 4594-4598, juin 1989, Genetics.

15 Le gène B-FIV de classe I est décrit dans Immunogenetics 31:405-409, 1990.

L'invention vise notamment les molécules d'acides nucléiques répondant à ceux des enchaînements de l'un des gènes suivants :

20 . enchaînement du système Rfp-Y

B-FV (figure 1), B-F VI (figure 2) ;

. enchaînement du système B,

25 8.4 génomique (figure 3) ; B-F I (figure 4) ; C12.1 (figure 5) ; DM (figure 6) ; TAP1 (du début de l'exon 2 à l'extrémité 3') (figure 7) ; et TAP2G (figure 8), et autres gènes compris dans la figure 10 et suites 1 à 35.

30 L'étude des séquences d'acides nucléiques des molécules définies plus haut a permis de repérer avec précision les blocs de polymorphismes qui doivent être détectés pour établir un génotypage fiable et précis.

En comparant les séquences de ces blocs, provenant de différents gènes d'un même haplotype ou d'un même gène de différents haplotypes, les inventeurs ont pris en considération les enchaînements divergents et élaboré, pour chaque gène, des oligonucléotides complémentaires de ces enchaînements divergents.

On dispose ainsi d'amorces spécifiques et discriminantes vis-à-vis d'un gène donné du système B ou du système Rfp-Y.

L'invention vise tout spécialement les molécules d'oligonucléotides correspondant à ces enchaînements et comprenant une partie de la région polymorphe des systèmes du CMH du poulet ou autres oiseaux d'élevage.

On rappelle que la région polymorphe peut être dans le gène ou dans une région apparentée telle que les régions microsatellitaires ou celle du promoteur.

Selon un mode de réalisation de l'invention, les polymorphismes sont liés à la fonction des systèmes du CMH.

Il s'agit ainsi avantageusement de molécules correspondant à une partie d'un exon. On citera à titre d'exemple des molécules correspondant à l'exon 2 (domaine α 1) des gènes YF du poulet. Un couple d'amorces approprié est constitué par :

Y-F VI α 1 : GGCCCCGGGATGCCGCGGTTC
Y-F VI α 1, R : ATCCGCTCACCGCCCTGG

Selon un autre mode de réalisation de l'invention, les molécules oligonucléotidiques correspondent à une partie d'une région polymorphe qui n'est pas liée à la fonction des systèmes du CMH. Des régions préférées de ce type sont des microsattellites.

En considérant par exemple, le gène B-FI, des molécules d'oligonucléotides utilisables pour constituer des couples d'amorces correspondent aux enchaînements suivants :

10 B-FI : 5' CCA GCA GTC ACT GCA CAT AT 3'
B-FI, R : 5' AGG TGG AGT GCG CAA AGT T 3', et
12.1 : 5' ACA CGC AGC AGA ACT TGG TAA 3'
12.1 R : 5' GGA AGG AAG ACC TTG GAA 3'

15 Avec les molécules oligonucléotidiques définies ci-dessus et celles élaborées à partir de gènes connus, mais selon la démarche de l'invention, on dispose de jeux d'amorces hautement spécifiques, permettant de déterminer avec précision l'haplotype de l'animal à étudier et de
20 détecter s'il est résistant au développement de tumeurs viro-induites, ou au contraire susceptible d'être affecté.

L'invention vise donc également une méthode de
25 génotypage d'oiseaux d'élevage et notamment du poulet.

Cette méthode est caractérisée en ce qu'elle comprend

- l'amplification d'un échantillon d'acide
30 nucléique provenant de l'animal à étudier à l'aide d'un ou de plusieurs couples d'amorces capables de s'hybrider spécifiquement avec l'acide nucléique d'une région polymorphe des systèmes Rfp-Y ou B du CMH desdits oiseaux,

et

- la détection des produits de PCR obtenus.

Une simple comparaison des résultats obtenus avec un référentiel établi au préalable permet de
5 déterminer rapidement l'haplotype de l'animal.

L'échantillon d'acide nucléique est constitué en particulier par de l'ADN génomique extrait de matériel biologique de l'animal à étudier ou par ce matériel même, en particulier par du sang de l'animal. Il peut s'agir en
10 variante d'ADNc, d'ARN ou encore de PNA (polypeptides nucleic acids).

Les amorces sont élaborées à partir des molécules oligonucléotidiques définies ci-dessus et,
15 d'une manière générale, de tout gène (et région apparentée) codant pour une protéine impliquée dans le contrôle de la résistance ou de la susceptibilité aux tumeurs viro-induites chez les oiseaux d'élevage et notamment de poulet, en particulier les gènes B-L de
20 classe II, 17.5, 12.3 et B-FIV de classe I.

Il s'agit par exemple d'amorces de régions microsatellitaires permettant de détecter des haplotypes du complexe B, telles que celles élaborées à partir du gène B-FI, et évoquées ci-dessus, ou d'amorces permettant
25 de détecter des haplotypes du système Rfp-Y, et élaborées à partir du gène 17.5, comme le couple :

17.52 : CAG GAT CTG CAC TGG CCA ATA

30 17.5, R1 : GAA TGG CGG TGC TTC CGT GCC TGG

La détection des produits de PCR est effectuée selon les techniques classiques. Ces techniques

comprennent le séquençage, l'électrophorèse, les hybridations avec analyse SSOP ou SSCP.

5 Cette technique sera avantageusement choisie selon la nature du polymorphisme impliqué. Ainsi, dans le cas de polymorphisme de type microsatellite, on détectera avec avantage les produits de PCR selon leur taille en ayant recours aux techniques d'électrophorèse.

10 Lorsque le polymorphisme ne concerne que quelques nucléotides, voire un seul nucléotide, on aura plus spécialement recours, aux fins de différenciation des haplotypes de produits de PCR, aux techniques d'hybridation (analyse sur membrane à l'aide de sondes
15 spécifiques des séquences d'haplotypes, SSOP ou Sequence Specific Oligonucleotide Probe), de migration différentielle des échantillons dénaturés (SSCP ou Single Strand Conformational Polymorphism), ou de séquençage. De manière générale, cette dernière technique est préférée
20 compte tenu de la simplicité de sa réalisation.

L'invention fournit ainsi une technique simple et rapide d'établissement du profil génétique d'un grand nombre d'animaux à étudier, ce qui permet de déterminer
25 les haplotypes et de sélectionner ceux d'intérêt en vue d'un élevage.

De plus, chaque type de gène pouvant être discriminé en utilisant des amorces présentant la
30 spécificité requise et son appartenance au système B ou Rfp-Y pouvant être établie, il est possible d'effectuer des études fondamentales plus complètes.

L'invention vise également un coffret ou trousse pour détecter le génotype du poulet ou autre oiseau d'élevage selon la méthode définie ci-dessus.

5 Ces coffrets ou trousse sont caractérisés en ce qu'ils comportent les réactifs nécessaires pour la réalisation d'au moins une PCR et du test de révélation.

10 En particulier, ils comportent les amorces pour la PCR, un témoin positif de la réaction, ainsi qu'une notice d'utilisation.

15 Les amorces se présentent sous forme lyophilisée ou en solution ou, selon le mode de détection, sur un support. Le support peut être, de manière classique, une plaque multipuits ou se présenter sous forme de puces à ADN.

20 L'invention vise en outre un système expérimental qui permet d'étudier la résistance au développement tumoral chez le poulet.

25 Il s'agit de lignées d'animaux qui ont été triées génétiquement sur leurs caractéristiques du CMH. En fonction de ces caractéristiques, les lignées sont soit résistantes, soit sensibles vis-à-vis des tumeurs induites par des virus, comme le virus de la maladie de Marek. Cette sélection génétique, qui s'est dans un premier temps effectuée sur des critères sérologiques, a
30 été ensuite poursuivie sur la base de l'étude du polymorphisme des gènes du CMH. Il s'agit d'un matériel génétique qui est parfaitement défini d'un point moléculaire, et constitue un outil précieux pour l'étude du polymorphisme des séquences de type microsatellite. Ce

matériel, ainsi que le produit du croisement entre certaines des lignées entre elles, a été utilisé pour déterminer les séquences microsatellites du CMH qui sont polymorphes et pour évaluer si ce polymorphisme peut être
5 corrélé avec les données de typage déjà disponibles pour ces lignées.

D'autres caractéristiques et avantages de l'invention sont exposés dans les exemples qui suivent, dans lesquels il est fait référence à la figure 9
10 représentant une photo d'électrophorèse de produits de PCR illustrant le test de génotypage de l'invention. On rappelle que les figures 1 à 8, déjà évoquées ci-dessus, illustrent les séquences de gènes selon l'invention.

15

Exemple :

Etude d'haplotypes Rfp-Y du poulet à l'aide d'amorces microsatellitaires.

20

- amplification avec le Kit Expand™ High Fidelity PCR System

. Avec les amorces 17.5 R1/17.52

25

ADN génomique : 1 µg

Oligos prendre : 0,3 µM

dNTP : 8 µl

qsp H₂O 50 µl

30

On ajoute 50 µl de Mix 2 en mélangeant.

Mix 2 : 0,75 µl d'enzyme

10 µl TP10X avec MgCl₂

qsp H₂O 50 µl

Programme d'amplification :

30 Cycles

5

94°C	94°C	65°C	72°C	4°C
2'	30''	1'	1'	∞

. Avec B-FI/B-FI, R :

10

ADN génomique : 1 µg

Oligos prendre : 0,3 µM

dNTP : 8 µl

qsp H₂O 50 µl

15

et ajouter 50 µl de Mix 2 en mélangeant.

Programme d'amplification :

30 Cycles

20

94°C	94°C	60°C	72°C	4°C
2'	30''	1'	1'	∞

25 - révélation par électrophorèse sur gel
d'agarose ou par séquençage.

30 Le test a été appliqué à 9 haplotypes de
poulet, sélectionnés sérologiquement pour le complexe B.
Il s'agit des haplotypes B4, B5, B7, B12, B13, B14, B15,
B21 et d'un haplotype inconnu BX.

Plusieurs individus d'un même type ont été
étudiés pour B12 (6 individus), B13 (3 individus), B14 (4

individus), B21 (4 individus) et un seul individu pour les autres haplotypes.

5 La figure 9 donne une photo d'électrophorèse sur gel d'agarose à 1 % des produits de PCR obtenus à l'issue de l'étape d'amplification.

10 Les pistes 1 et 27 correspondent aux marqueurs de taille et les pistes (2 à 25) aux produits de PCR des haplotypes suivants : piste 2 : B4 ; piste 4 : B5 ; piste 5 : B7 ; pistes 6 à 11 : B12 ; pistes 12, 13, 14 : B13 ; pistes 15, 16, 17, 18 : B14 ; piste 19 : B15 ; pistes 20, 21, 23, 24 : B21 ; piste 25 : BX (absence de détection pour les pistes 3 et 22).

15 L'examen de cette figure montre que les individus qui ont l'haplotype B12 donnent une même bande et sont donc bien homogènes. La même observation s'applique aux individus B14. En revanche, avec B21, on constate que les profils sont différents, ce qui démontre
20 l'inefficacité de l'approche sérologique. Compte-tenu de la position de la bande de BX, on détermine qu'il s'agit d'un haplotype B4.

25 L'application pratique de cette méthode revient à soumettre les individus naturellement résistants au protocole décrit ci-dessus en prenant en compte les deux systèmes Rfp-Y et B du CMH et à ne sélectionner parmi des animaux à tester que ceux dont le profil correspond à celui des animaux résistants.

30 L'invention fournit ainsi les moyens de vérifier l'homogénéité des animaux et d'effectuer des sélections rigoureuses en prenant en compte chaque système du CMH, et dans ces systèmes les gènes recherchés.

REVENDEICATIONS

1/ Molécules d'acides nucléiques isolées de leur environnement naturel, de gènes codant pour des protéines impliquées dans le contrôle de la résistance ou de la susceptibilité au développement de tumeurs chez le poulet, telles que celles de la maladie de Marek, et de régions apparentées auxdits gènes caractérisées en ce qu'elles présentent les séquences d'acides nucléiques de gènes du système B ou du système Rfp-Y, correspondant au complexe majeur d'histocompatibilité des oiseaux d'élevage à l'exception des séquences des gènes de classe II B-L, du gène 17.5, du gène 12.3 et du gène B-FIV de classe I, ou sont capables de s'apparier avec l'un des brins d'un gène capable de coder pour une protéine telle que définie ci-dessus dans des conditions faiblement stringentes.

2/ Molécules d'acides nucléiques selon la revendication 1, caractérisées en ce qu'elles répondent à l'un des enchaînements suivants :

. enchaînement du système Rfp-Y

B-FV (figure 1), B-FVI (figure 2) ;

. enchaînement du système B,

8.4 génomique (figure 3) ; B-FI (figure 4) ; C121 (figure 5), DM (figure 6), TAP1 (du début de l'exon 2 à l'extrémité 3') (figure 7), et TAP2G (figure 8).

3/ Molécules d'acides nucléiques selon la revendication 1 ou 2, caractérisées en ce qu'elles correspondent à une partie des séquences définies dans les revendications 1 ou 2, cette partie étant spécifique

et discriminante pour un gène donné des systèmes B et Rfp-Y.

5 4/ Molécules d'acides nucléiques selon la revendication 3, caractérisées en ce qu'il s'agit de molécules d'oligonucléotides correspondant à une partie de région polymorphe des systèmes du complexe majeur d'histocompatibilité du poulet.

10 5/ Molécules d'acides nucléiques selon la revendication 4, caractérisées en ce qu'il s'agit de molécules d'oligonucléotides correspondant à une partie d'exon.

15 6/ Molécules d'acides nucléiques selon la revendication 4, caractérisées en ce qu'il s'agit de molécules d'oligonucléotides correspondant à une partie de région polymorphe qui n'est pas liée à la fonction des systèmes du CMH, telle que les régions
20 microsateellites.

7/ Méthode de génotypage d'oiseaux d'élevage et notamment du poulet, caractérisée en ce qu'elle comprend

25 - l'amplification d'un échantillon d'acide nucléique provenant de l'animal à étudier à l'aide d'un ou de plusieurs couples d'amorces capables de s'hybrider spécifiquement avec l'acide nucléique d'une région polymorphe des systèmes Rfp-Y ou B du CMH desdits
30 oiseaux,

et

- la détection des produits de PCR obtenus.

8/ Méthode selon la revendication 7, caractérisée en ce que les amorces sont élaborées à partir des molécules selon l'une quelconque des revendications 3 à 6, et de tout gène (et région apparentée) codant pour une protéine impliquée dans le contrôle de la résistance ou de la susceptibilité aux tumeurs viro-induites chez les oiseaux d'élevage et notamment de poulet, particulièrement les gènes de classe II B-L, 17.5, 12.3 et B-FIV.

10

9/ Méthode selon la revendication 7 ou 8, caractérisée en ce que la détection des produits de PCR est effectuée par séquençage.

15

10/ Coffret ou trousse pour le génotypage d'oiseaux d'élevages et notamment du poulet, caractérisé en ce qu'ils comportent les réactifs nécessaires pour la réalisation d'au moins une PCR et du test de révélation, selon la méthode de la revendication 8 ou 9, en particulier les amorces élaborées à partir des molécules d'acides nucléiques selon l'une quelconque des revendications 3 à 6.

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Figure 1BF V

B-F V

GGC CCC GGG ATG CCG CGG TTC GTG ATC GTC GGG TAC GTG GAC GAC AAA ATC TTC GGT
ACC TAC AAC AGT AAG AGC AGG ACT GCA CAG CCT ATC GTG GAG ATG CTG CCG CAG GAG
GAC CAG GAG CAC TGG GAC ACG CAG ACC CAG AAG GCG CAG GGC GGT GAG CGG GAT TTT
GAC TGG AAC CTG AAC AGG CTG CCG GAA CGC TAC AAC AAA AGT AAA GGT GAG CGT GGG
GGA AGC TGC AGC GCG ATG CGT CTG GGA CAG GAG CTC TGT GTG CCG AGG GTG TCC GCC
AGC CCC ACT GAG GTG TGG CCG TGC CCC ACG CCC AGC TGT GCT GGG CCG TCC ATG TGT
GGT GGC ACT GTC CCT GGG CCG CCC TGC TCC TGC GCC CAC CCA CCC CAC CCC AGC CTC
ATG GCA CTC GCG GTG CCC CAC AGC CCT AGA AGC CTC TCA CCT ATT ACT CTG GCT GTG
CCT CAG GGT CTC ACA CGA TGC AGA TGA TGT TTG GCT GTG ACA TCC TGG AGG ACG GCA
GCA TCC GAG GGT ACG ATC AGT ATG CAT TTG ATG GGA GGG ACT TCC TTG CCT TTG ATA
TGG ACA CGA TGA CGT TCA CCG CGG CGG ATC CAG TGG CTG AAA TCA CCA AGA GGA GAT
GGG AGA CAG AAG GGA CGT ATG CTG AGA GAT GGA AGC ATG AGC TGG GGA CTG TCT GTG
TTC AGA ACT TGA GGA GAT ACC TGG AGC ATG GGA AGG CAG CGC TGA AAA GGA GAG GTG
AGG ATG GGA GGG GGA CGT GGG GCT GGG CTG GGT GTG GGG CAG AGG CTC AGT GTG GGG
TGC TCA GCC CCG CCC ACA ACG TCA CCC ACC TGC AGT GCA GCC CGA GGT GCG AGT GTG
GGG GAA GGA GGC CGA TGG GAT CCT GAC CTT GTC CTG CCA CGC TCA CCG CTT CTA CCC
GCG GCC CAT CAC CAT CAG CTG GAT GAA GGA CGG CAT GGT CCG GGA CCA GGA GAC CCG
CTG GGG GGG CAT CGT GCC CAA CAG CGA TGG CAC CTA CCA CGC CTC GGC TGC CAT TGA
TGT GCT GCC GGA GGA TGG GGA CAA GTA TTG GTG CCG CGT GGA GCA CGC CAG CCT GCC
CCA GCC TGG TCT CTT CTC ATG GGG TGA GCT GGC AGC GTG GGG CAC GTG GGG TTG GGA
TTC GCA GGC TGC CCC TTC CTT TAC TGA CAA CGG CGC TCT CCT CCA GAG CCG CAG CCC
AAC CTG ATT CCC ATT GTG GCA GGG GCG GTC GTT GCC ATC GTG GCT GTC ATC GCT GCG
GTC GTT GGA TT

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Figure 2B-FVI

GGC CCC GGG ATG CCG CGG TTC GTG ATC GTC GGG TAC GTG GAC GAC AAA ATC TTC GGT
ATC TAC GAC AGT AAG AGC AGG ACT GCA CAG CCC ATC GTG GAG ATG CTG CCG CAG GAG
GAC CAG GAG CAC TGG GAC GCG CAG ACC CAG AAG GCC CAG GGC GGT GAG CCG GAT TTT
GAC TGG TTC CTG AGC AGG CTG CCG GAA CGC TAC AAC AAA AGT GGA GGT GAG TGT GGG
GGA AGC TGC AGC GCG ATG CGT CTG GGA CAG GAG CTC TGT GTG CCG AGG GTG TCC GCC
AGC CCC ACT GAG GTG TGG CCA TGC CCC ACG CCC AGC TGT GCT GGG CCG TCC ATG TGT
GGT GGC ACT GTC TCT GGG CTG CCC TGC TCC TGC GCC CAC CCA CCC CAC CCC AGC CTC
ATG GCA CTC GCG GTG CCC CAC AGC CCA AGA AGC CTC TCA CCT ATC ACT CTG ACT GTG
CCT CAG GGT CTC ACA CGA TGC AGA TGA TGA TCG GCT GTG ACA TCC TGG AGG ACG GCA
GCA TCC GAG GGT ACG ATC AGT ATG CAT TTG ATG GGA GGG ACT TCC TTG CCT TTG ATA
TGG ACA CGA TGA CGT TCA CCG CGG CGG ATC CAG TGG CAG AAA TCA CCA AGA GGA GAT
GGG AGA CAG AAG GGA CGT ATG CTG AGA GAT GGA AGC ATG AGC TGG GGA CTG TCT GCG
TTC AGA ACT TGA GGA GAT ACC TGG AGC ATG GGA AGG CCG CAG TGA AAA GGA GAG GTG
AGA ATG GGA GGG AGA CGT GGG GCT GGG CTG GGT GTG GGG CAG GGG CTC AGT GTG GGG
TGC TCA GCC CGG CCC ACA ACA TCA ACC ACC TGC AGT GCA GCC CGA GGT GCG AGT GTG
GGG GAA GGA GGC CGA TGG GAT CCT GAC CTT GTC CTG CCA CGC TCA CCG CTT CTA CCC
GCG GCG CAT CGC CAT CAG CTG GAT GAA GGA CAG CAT GGT CCA GGA CCA GGA GAC CCG
CTG GGG GGG CAT CGT GCC CAA TAG GGA TGG CAC TTA CCA CAC TTC GGC TGC CAT TGA
TGT GCT GCC GGA GGA TAG GGA CAA GTA TCG GTG CCG CGT GGA GCA CGC CAG CCT GCC
CCA GCC TGG CCT CTT CTC TTG GGG TAA GCC TGG CAG CGT GGG ATG TGT GGA GTT GGG
ATT TGG GGG CCG CCC CTT TGT TTA CTG ACA ACG GTG CTC TCC CCC AGA GCC GCA GCC
CAA CCT GAT CCC CAT TGA GGC TTG GCT GGT CGT CCC CTT GGT GGT TCT CTT CGT TGC
TTT GAT TGC ATT

GGA TCC GGG GTG GGT GGC AGT GGC TGT GTT TAG GTC GGC CTG TGG GGA AAG
 CCG GGT TGT CCC ACC CAT GTC CCC TCT TCC AAC ACT GTT CCT GAA TGA GTT
 TTC CCT CTC CGA CCC TTT TTT TAA TGG GTT TCA GGG ATT TAA AAT TAA TAT
 TGA CGA AGT GAC GGA GGG GGT GGG GCC ACA GCG GAG CCG AAA GCG AAA GCA
 GCG GAG AGC AAT GGC TGC GGG GCT GCG GCT GCT GCT GGC GGG TGA GAC CCG
 ACC CCC CCC GGC CCC CTC ATG TCC CAC CAC CCA TAT CGC CCC CCC CCC TCC
 TCC TCG CCC CAT GCT GAG CCT CTC CCC CAC CCC CAG GGC TCT GCT GGT CCC
 AAT TTA GGG TGG AAG ACG CCG CCT CCC CTC CGC CCC CCC CCG CTC CGG TGC
 GCT GCG CGC TGC TGG AGG GGG TGG GGC GCG GGG GAG GGC TGC CGG GGG GGG
 GCA ATG CCC GTC CTG CAC TGC TGC GCT TTG GGG GGG ACG CGG AGA CCC CTC
 CCG AAC CCG GCC CGG AGC CCG AAG TCA CCT TCA ATG TCA GCG GTA CGT GGG
 GAC CCC CGT CAC TGT GCT GTG CGC CTC CTT TAT CCC CAC CCC CCT CCA TGT
 CCC CAT CTC CTT TAC TTC CCA CAA TGC TCC CAT CCC CCC CAG AAT GTC CCC
 AGA GTC CCC CAA ACC CCC ATG ACC CCC CCC ACG ACC CCT GGT TCC CAT TAC
 CCT CTC ACG TCC CCC AGT GTC CCC AAG ATT CCC ATT ACT CCC CGT ATC CCC
 ATT ATC CCC AAA ATG TCC CCC AAT GTT CCC ATC ACC CCA ATG TTC CCA AGG
 TCC CTA TCG CTC CTC AAT GTC GCT ATG ATC CCT ATT CCC AAA ATG TCA CCA
 ATG TCC CCA AAA TCC CCA TTA TCT CCC ACC TCT CCA AAG TCC CCA AGA TCC
 CCA TTA CCC CCA ATA TCC TCA TTA CAC CCC AAA TGT CCC CAA TGT CCC CTC
 CAT GTC CCC CAG AGA CCC CAT TAG CCC CAA TAG CTC CCA AAC TGT CCC CAG
 TGT CCC CAT TAA CCC CAA AAT GAC CCC ATT ACG CCC CAC ACC CCT CCC AAC
 CCC ATG CCC TCA GAC CCC TTC ATC CCT CTC ACT CCT CTC TCC CTC GCA GAC
 CCC TGG GGG ACT CTA GCC CCA CTC GGG TCC CCC CCC GGA CTC CCC CCA GCT
 GCG AAC TGA ACC CCA CGA ACC CCC AGA CCG GCT CTG ACC CAT GGA GCC GCC
 CTC TGC ACC CCG ACG CCC GCA GCC CCC CAA CCG CGG GGG GGC AGT GGT GGG
 TGG CGG CGG TGG GGA CCC CGC AGT ACG GTG TCA CTG CGC TGC TGC AGG GGG
 GGA TGG GCA CAG AAG GAA CCA TCA CTG CCG CCG GTA AGG GGG AAC TTG GGG
 TGT CCC TCC CTG GGT GTC CCC ATG TCC CTA TCT GTC CCC CAG TGT GTC CCC
 ATT TGT CCC CTC CTC TGC ATG TGT CCC AAT GTC TCC ATA CAT CCC ATA ATA
 ACC ATA TGT CCC CAC TCA TCC CCA TAT TCC CCA TGT GTC CCC ATA TCC CCA
 CAC ATC CCA GTG TGC CCC AAC ACA TCC CCA TGT GCC CCC CCC CAT GCA TCA
 CTA CCA TCC CCC TAT CCC CCA AGT GTC CCT GTG TCC CTG CAG TTT CTC CCT
 GTC CTC ATG TGT TCC CAT GTC TCC ATG TCA CTG TGT CCC CGT GTC CCC ACA
 CAT CAC CAT GCC CCC CAC TGC AGC GCC CCC ATG TCC CTT CAC CTC TCC ATG
 TCC CCC AGT GTC CCC TAT CCC CTC ATT GTC CCC ATG CCC CCT CAC CTC CCC
 GTG TCC CCC GTG TCC CTA TGT TCC CCT GGT GTT TCC ATG TCC CCT CAT GCC
 CCC ATG TCC CCT CAT GTC CCC ATA TCC CCC AGT GTC CCC ATG TCC CTT CAC
 CTC CCC ATG TCC CCC AAT ATT CCC ATA TCC CCT CAC CTG CCC ATT TCC CCC
 CGA TGT TCC CAT GTC CCC GCA CCT CCC CAT GTC TTC ACA GTG GCC CTG GCG
 GTG CTC ACC CAC ACC CCG ACC CTC CGG GCC CGT GTG GGG TCC CCC ATC CAC
 CTG CAC TGC GCC TTC GCT GCC CCC CCA TCC TCC TTT GTC CTC GAG TGG CGT
 CAC CAG AAC AGG GGT GCG GGG AGG GTC CTG CTG GCC TAT GAC AGT TCC ACC
 GCC CGC GCC CCC CGC GCC CAC CCC GGG GCC GAA CTG CTG CTG GGG ACA CGG
 GAT GGG GAC GGG GTG ACA GCG GTG ACA CTG CGG CTG GCG CGG CCA TCA CCG
 GGG GAT GAG GGC ACC TAC ATC TGC TCC GTG TTC CTG CCC CAC GGG CAC ACA
 CAG ACA GTG CTG CAG CTC CAC GTC TTT GGT GCG TCC ATG TGG GGC AGG CGG
 TGT TCC TAT GGG GTG TGG GGT TGG GCA GTG TTC CTA CGG AGT GTG TAT GAC
 TGG GTG GTA TTC CTA TTG CTC AGA TAG GAC ATA TGG GAG CAG GCG GTA TTC
 CTA TGG GGC TGT AGG GTG GAT GCG ACT GCG TGA TAT TCC TGT GGG GGC TGT

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AGG GTG GAT GGG ACT GGG TGG TAT TCC TAT GGA GGC TAT AGG GTG GAT GGG
ACC GGG TGG TAT TCC TAT GAG GAC TAT AGG ATG GGG TGG CAT CAT CCC ATA
GTT CAC CTG TAG GTT TAT AGG GGG GGA TGA GCC CTA TAC AGC GTA TGG GCT
ATA TGG ACC GAT GTC CCC CCA CAT GTC TCC AGA GCC CCC CAA GGT GAC GCT
GTC CCC GAA GAA CCTGGT GGT GGC CCC GGG GAC GTC AGC AGA GCT ACG CTG
CCA GTC TGG CTT CTA CCC CTT GGA TGT GAC GGT GAC GTG GCA GCG CCG CGC
CGG GGG CTC GGG GAC ATC ACA GTC ACC CAG GGA CAC AGT GAT GGA CAG CTG
GAC TTC AGG TCA CCG CCA GGC AGC CGA TGG AAC CTA CAG CCG GAC GGC GGC
AGC ACG GCT GAT CCC CGC ACG CCC CCA ACA CCA CGG GGA CAT CTA CAG CTG
CGT TGT CAC CCA CAC TGC ACT GGC CAA ACC AAT GCG TGT CTC CGT CCG ACT
GCT CCT GGC TGG TGA GGG GGG ATG TGG GGA TAT TGG AAA CAC GTG GAG GTA
TTG GGA TGC TGG GAC CAT GGT TAG GAG GGT CTG AGG GAC ATC AGG ACC ATG
GCC TGG GAC AAT GGG AGA TCA TGG ATT TGG GTT GGG GAC CCC ACC CAG GAT
GGT GAC ACT GTG CTT AGG GCT GTC GTT GTC CCC ACA GGC ACC GAG GGA CCG
CAC CTG GAG GAC ATC ACG GGG CTC TTC TTG GTG GCC TTT GTC CTC TGT GGC
CTC ATC CGT TGG CTC TAC CCT AAA GGT GAG TGC TGT TCC CAC ATC CCA GTG
CCC CCA CAT CCT CAC ACC CCA ATA TCC CAA TGG CCC ATG TCC CCA TGA GCA
ATG TCA CTA TGT CCC AAT ATC CTA ATG ATG CTG TGT ACC CAT GTG TCC CCA
TGT CCC TAT TCC ACT CAC TCT TTC TCT CCC CTC AGC TGC ACG ACC CAA AGA
GGA AAC CAA GGT AAC ATT CCT CCC CAA AAA CCC CAA ATC CCC CAA AAC ACC
TCC AAG CAC CCC AAA ACT CAC CAT TCT CAT TCC CCC CCC CCC CCC CCC
CCC CAT GCC TTG CAG AAA TCG CAG TGA CCT CCA CTC CAG CTC TCA GCA CCT
CAG CTC CAG ATA AAG AGT TTT TCA CCC CAA AGT TAT ATA TGT GTG GTG GTG
TCC CCA CAG ATC TGG GTG CAG AGG GGG GAG AAA TGG GGG CAA ACT GGG AGC
AGT GGG AGC AGT GGG AGG AAG TCC TGG GTT GGT GAG GCA GAT GAG TGG CAC
CTG GGG ACA TCT GGG TGC CAT CCC TTG TGG ACA TCT GGG TGA CAC TGC ATT
GCC TTG GGT GAC ATT GGG ATC CTC AGG TCA CTG CAG

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Figure 4

B-FI

GT CGA CCGGAT CTGGATAGGT CGT CAGT CAT CCTAATTAAGGAGGGA CAA CAGTGAATGGG
 GAGGAG CCGATGA CT CAGG CTGGGAGTGGT GAT CCCAGAGGTTT CCT CTG CTGT CAGTGAC
 TCCGTG CTTT CGCTTT CGCTT CA CAA CCTGAGGGAG CG CATT CTGCCTGGCG CCCGATGAC
 GT CA CATAAA CCCCCGA CTGCCATTGG CGGAGAGG CGA CGGAGGAG CCAATGGGGG CGCGG
 GG CCGGG CGGAGGAGTAGGAAAAG CTGAAGGA CGTG CG CTGGGTG CGG CGGA CTGAGAGT
 GCAG CCGTGTGAGGCGATGGGG CCGTG CGGGG CG CTGGG CCTGGGG CTG CTG CT CG CGCC
 GTGTG CCGGG CGG CGG CCGGTGAGTG CGG CCGGA CCGGA CCCCT CCCCG CCTGTAA CCCC
 A CCCC GGG CTGTG CCGTGGGAT CCT CAGA CCCCCA CCG CGG CT CACGG CCT CG CTGCCG
 T CCG CCCCCG CAGAG CT CATT CCTTG CCGTA CGT CCATA CGG CGATGA CCGAT CCGGCC
 CCGGG CTG CCGTGGT TCGTGA CGTGGGGTACGTGGA CCGGGAA CTCTT CGTG CACTACAA
 CAG CA CCG CGCGGAGGTACGTG CCCCCA CCGAGTGGATGGCGG CCAACA CCGA CAG CAG
 TA CTGGGATGGA CAGACG CAGAT CCGA CAGGG CAATGAG CCGAGTGTGGAAGT GAG CTGGA
 A CACA CTG CAGGAA CGATA CAA CCAGA CCGG CCGT GAG CA CGG CCGGG CCG CGG CT CCGT
 GGGTGTGGGATGGG CT CATGG CG CAGT GCG CCA CCA CCCCCAGG CCTGG CCTG CCGG
 G CGG CACCGT CCGGGG CTG CCGGT CACAG CCCCCA CCG CG CT CCGGGT GCG CGT CCGGG
 GGA CCCCCA CCGAT CCGG CTG CAGTGGGAG CCGGAG CCGAGGGG CCCCT CACCCCCT
 G CCGG CTGTGTTT CAGGGT CT CAAA CCGTG CAG CTGATGTACGG CTGTGACAT CCT CGAG
 GATGG CACCAT CCGGGGGTAT CAT CAGA CAG CCA CAGATGGGAGAGA CTT CATTG CTTT CG
 A CAAAGG CACGATGACGTT CACTG CGG CAGTT CCAGAGG CAGGTT CCA CCAAGAGGAAAT
 GGGAGGAAGGAGGTGTTG CTGAGAGGTGGAAGAGTTA CCTGGAGGAAA CCTG CGTGGAGGG
 GCTG CCGAGATA TGTGGAATA CCGGAAGG CTGAG CTGGG CAGGAGAGGTGAG CCGGGT CGG
 GGTGGGGGGGGGGGGGGG CGGACG CAGTGTGGGGT CGGACGTGGGG CCGGGG CT CAT CGTG
 GGGAG CT CAG CCGGCCCT CACTG CCG CCA CCA CAGAG CCG CCTGAGGTG CAGTGTGG
 GGAAGGAGG CTGA CCGGAT CCTGACCTTGT CCTG CCG CG CT CACGG CTT CTA CCG CGG C
 CCAT CG CCGT CAG CTGGCTGAAGGACGG CG CCGTG CCGGG CAGGACG CCCAGT CCGGGGG
 CAT CGTG CCAACGG CGA CCG CACCTA CCA CACCTGGGT CACCAT CGATG CG CAG CCGGGG
 GACGGGGACAAGTACAGTG CCG CGTGGAG CACG CAG CCG CCGG CCTG CCGG CCT CTA CT
 CGTGGGGT GAGT GAGGGGATGTGGGG CTGGGGGG CTG CCGG CTG CCCCTT CCCCTG CTGAT
 GG CCGG CT CT CCCCCAGAG CCG CCA CAG CCAACCTGGTG CCCAT CGTGG CCGGGGTGGC
 CGT CG CCA TTGTGG CCA CT CG CCA CTG GGT TGGT TGGATT CAT CAT CTA CAGACG CAC
 G CAGGTAAAAG CAGAGGGTG CAGG CCGG CAGTGGGG CTGTAGGGGGAT CTGGGT CCCCC
 CTTGGGAG CCCCCA CCGTGTGTGATGTGAACCTGTGATGAAGCAT CT CT CTT CTG CAG
 GGAAGAAGGGGAAGGG CTA CAA CAT CG CG CCGGTGAGT GATGAGGG CAG CG CTGT CCCCC
 ACCT CTG CCCAGTG CCAGGGTGGT CCTGGGGT CCTG CTTT CT CCAAGGTACCCATT CCT
 GGTG CTTGGGG CTG CT CCA TG CCCCATAGGGAG CACAGGG CTGGAT CT CACAG CTGTT CCT
 CCCTTATAGA CAGGGAAGGTGGAT CCAG CAG CT CGAG CACAGGTG CCGTGTGGGG CTGTGG
 GTTGGGAGGGGT CCGTGTG CT CT CTGTGGTA CTGCCAGGG CTGGG CTATG CTGGGG CT CT
 GCGGGGAGAC CCGGAG CAGAGGGT TGGGATGTGAA CCTGG CCGGTGGGACAT CAT CCC
 TT CT CAT CCA CAGGGAG CAA CCG CCA CTGAGTG CTGTGCTT CAG CCGT CAGGAG CC
 AACAGT CACACAG CATT TGGGGT CCGTGTGGA CACAG CCGCAT CCT CCGT GACCT CT CA
 CAT CT CATT CTG CTT CCTATG CTGA CTGTTATG CTTTG CCGT GACTG CTT CCTGTGAAATA
 AAATGATGGG CATT CTGTGCT CAG CTTG CCTG CATT CTG CACAGTG CTGTGGTTGGGGAT
 GGGGTGGGTGAGAGGA CCGTGT CAGT TGG CTG CT CAGGGTGCAGATGTGG CCCTGTGCT
 GAGTAC CCACTG CCCT CCCCCCTAT CTG CCTG CTG CT CACT CCCCCCT CCGTAC CCCCCAT
 CCCTT CT CACCT CT CCGTGTGAAC CCGATG CTGGTGGT TG CTGTGCT CCCTGT CCTGG CAG
 AACT CT CATT TT CCAATGGCAT CCCTGGGTGTGGGATGTGGT CT CCTTGGT CCT CCCCC
 CAG CAGT CACTG CACATAT CCCCCCACTT CCCCCCTAGGT TGTGT CCA CAG CACT CCT
 ATTT CCCT CT CCG CCCCCCCCCCCCCCCCCCG CCGCAT CAG CTG CCT CTG CAAT CCT CAC
 CCTTG CCGACA CAA CTTT TG CG CACT CCACT CCCT CAT CCG CCGCTT CCCCCAG CT CT C
 CTGT CCCTGCTGG CCCCCCT CCCCCCCCCCAT TGTACCTA CACCCAATAAATATGTTT
 GTTCTG CTGCCCT CAG CCGT CT CCGGTTTATTT CCCCCGATTGTGTGTGGGG CG

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TCCGCTCTTCACCCTGGGGGGAAGGGGCTCTGGGGGTCCCTCATTCTCCCTGCACTTCTTA
CAGCACCGGGA CTCCGCGCTGAGATCCCATCACACCGGGTACAAACATGCGGCTTTATT
CCCAGTTCTGTGTCCCACCCCCGGCCCTGGTGGCACTCAGTGGCACCGCAGTCCATGCAGT
GGCCGTTGTGTGTGTGTACAGCAGCGGTACC

12.1

Figure 5

ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGC
ACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCCATAGTTGCCTGCAAC
TCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCC
AGTGCTGCAATGATACCGCGAAGACCCACGCTCACCGGCTCCAGATTTAT
CAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCA
ACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT
AAGTAGTTCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCTGCAG
GCATCGTGGTGTACGCTCGTCTGTTTGGTATGGCTTCATTAGCTCCGGT
TCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGC
GGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCGAG
TGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTG
CCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATT
CTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACAC
GGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGA
AAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATC
CAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTA
CTTTCACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCA
AAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCT
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGAT
ACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA
TTTCCCCGAAAAGTGCCACCTGACGCTAAGAAACCATTATTATCATGAC
ATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAAT
TCCCGCCCGTAGCGCGCGCGCACCCAGCCGGCATCGCACCCGAGCACCAGC
TCCCGCGTCGTCCAGATGCCACGGGCCACGTCGAGGCCGACGGGGAGAA
ATACACGTACCTACCTGGGGATCTCAACAGGCCCCGGGTGGCCAACCAGG
TCGTGGACGCGTTGTGCAGGTGCGTGATGTCCAGCTCCGTCTCGGGTGC
CGCCGGGCCCCAACCGGGCGGTGCGGGGGGGCGGTGTATCACGCGGCCCGCT
CGGGTGGCTCGCCGTCGCCACGTTGTCTCCCCGCGGGAACGTCAGGGCCT
CGGGGTGAGGGACGGCCGAAAACGTTACCCAGGCCCGGGAACGCAGCAAC
ACGGAGGCGGCTGGATTGTGCAAGAGACCCTTAAGGGGGGCGACCGAGGG
GGGAGGCTGGGCGGTGCGCTCGACCGTGGTGGGGGGCGGGCAGGCTCGCGT
TCGGGGGGCGGCCGAGCAGGTAGGTCTTCGGGATGTAAAGCAGCTGGCCG
GGGTCCCGCGGAAACTCGGCCGTGGTGACCAATAACAAAACAAAAGCGCTC
CTCGTACCAGCGAAGAAGGGGCGAGAGATGCCGTAGTCAGGTTTAGTTCTG
CCGGCGGCGCCAGAAATCCGCGCGGTGGTTTTTGGGGGTGCGGGGTGTTT
GGCAGCCACAGACGCCCGGTGTTCTGTCTGCTCAGTCCAGTCGTGGA
GCCAGGCCATCCAAAAACCATGGGTCTGTCTGCTCAGTCCAGTCGTGGA
CCTGACCCACGCAACGCCCAAAATAATAACCCACGAACCATAAACCA
TTCCCCATGGGGGACCCCGTCCCTAACCCACGGGGCCCGTGGCTATGGCA
GGGCTTGCCGCCCCGACGTTGGCTGCGAGCCCTGGGCCTTACCCGAAC
TGGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGTATTGGCCCCAAT
GGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGAACCCCG
CGTTTATGAACAAACGACCCAACACCGTGCGTTTTATTCTGTCTTTTTAT
TGCCGTCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAG
TTAGCCTCCCCCATCTCCCGGGGTGGGCGAAGAACTCCAGCATGAGATCC
CCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCC
CAACCTTTCATAGAAGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGT
TGGGCGTCTGCTTGGTCCGTCTTTCGAACCCAGAGTCCCGCTCAGAAGA
ACTCGTCAAGAAGGCGATAGAAGNNN

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TGGGGTCTCTTTGGTCTGATGGAGAGAGGTTGGCACCAAGGTAAGTCGC
TGCCTACATCACCCTGGTGTCTCTCAGCAGCTGGTGTAATTTCTG
CCATCTGGGCTATTTCTGTAGAAAGCAAAGAAGCTCTGCTGGTGGGCAGC
TCATCTCCAGTGTGAAAAAGCAAATGCAACGCATGCACCCTGCTATCC
ATGTGGBCCYAKCCCTCTCCATCAGCTGTTGAAGGAGAAATCTGCACTCA
GAAGAGATTGAATTGGGCTCAGATCTGGCTTGGGAAGATGATGATTCCAA
CCAGAGTCCAGGAGACTTTGGGGAATGCATGAATCCTATAGGAAAATGGA
TAACCCTTCATCCAAGAGCAAGCTGGCATGATGCTCTGGGGTGAAAACCC
ATAATGCCACCTGGTTTTAAGGTTTGGGGTGGCTTACAATGTGCAGCTCT
GCTTCCGGCGAGGCACTGGGAGCCCTAAACCCATGGAGAGGTCAAACCAG
TGCTGGAGGTCATTGTGGGCCAGCTGCAATGGGAGGTAGGCAATTATGG
ACATCGCTGAAGCCACCCACGCTCTGGGGAACCTTGGGTTTTACCTTTC
ACTGCACTTTAATGGGATTTCTCATCAATGTCTGCATGTTCTTGGCCACC
TGTTTAAAAATATAATAATAATAATTAAATCTTTTGGCCCACTGCGGGAT
GAGCAGCTGGTGGTTCCAGCTCACAATAAACCACACTTGAGACTCCCTG
GAGAATTCGCTTTCTTTTGCAGCTGGTTCCATGTKGGGSYKTTACGCC
CTCTGCAGCTCATAGGCTTTTCTTACAGCCTCTGCTCCACCTATTGCTG
AAAAGGGGGAAATTTGAGATGGATCCCATTTTGTGAACATCTCCCMACCT
GTGGGTAAATGCTCAGACCTCTCAGCCCTGTGGGTTTAATTTCTCTTTCTG
CAGCTTAATGGGTTGGGGATGTTCACTACTGCAATAATTAGTGATGGGAT
AGGGGAGGCAGGAGAGGATCCCGTCGACCGATGCCCTTGAGAGCCTTCAA
CCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCAC
TTATGACTGTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCG
CTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGAT
CGGCCTGTCGTTGCGGTATTTCGGAATCTTGACGCCCCCTCGCTCAAGCCT
TCGTCAGTGGTCCCGCCACCAAACGTTTTCGGCGAGAAGCAGGCCATTATC
GCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTTCGCGAC
GCGAGGCTGGATGGCCTTCCCCATTATGATCTTCTCGCTTCCGGCGGCAT
CGGGATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACC
ATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCG
ATCATTGGACCGCTGATCGTCACGGCGATTTATGCCGCTCGGCGAGCAC
ATGGAACGGGTTGGCATGGATTGTAGGCGCCGCCCTATACCTGTCTGCC
TCCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAATG
GAAGCCGGCGGCACCTCGCTAACGGATTACCACTCCAAGAATTGGAGCC
AATCAATTCTTGCAGGAACTGTGAATGCGCAAACCAACCCTTGGCAGAA
CATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACGCGGCGCATCTCGG
GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCA
CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA
GATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG
ACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGT
GGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTG
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[illegible]

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Figure 6DM

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 CATGGGTTCTGTTCTCTGCATGCCCTCCACTGTCACTCCACATGCCACCGTCCCTTTATGTCCCTCCATCCCTCCACGTTGTTCTTTG
 TTCCCTCCATACATGCACTGTCCCTCCCTCCAGCCCTCCATTTCCCTTCCACCGCCCTGCAATGACACTGCTGTCCCCAG GCC CTG GCA
 CCA CAG ATG CAG AAG GCG CAG GCC CGG GCC AGC GAG GTG GCA GTG GAG ACC TTC CAG GCC ATG GCC ACT
 P Q M Q K A A Q A R A S E V A V E T F Q A M A T
 GTG CGC AGC TTT GCC AAT GAG GAT GGG GCA GCT GCA CAC TAC CGG CAG CGC CTG CAG CAG AGC CAC CGC
 V R S F A N E D G A A A H Y R Q R L Q Q S H R
 CTG GAG AAA AAG GAT GTG GCC CTC TAC ACT GCC TCT CTC TGG ACC AGT GGT GTATGGGATGGGCTGGCTCAAT
 L E K K D V A L Y T A S L W T S G
 AGCATGGGACGTGATGGGATGGGCTGGGGATGIGGGACATGATAGGATAGGACTGGGGGCATGGGGACATGGTGGGATAGGGCTGG
 GAGATGTGGAGACGTGATGTAATTGAGATGTCAGGRGATGGGACAGAAATGCCAACGGGCTGGAGGCCATATGTTGTGGAGATGGCAGGT
 CATGGGAATATGATGGGACTGTGGGACATAGATTTGATGGCATGGGACATCAGGATGTAGCAGGCAACACAGTTTCAGGGGCTCT
 GGGCAGGAGATGCAGTGACGTGGGATGGGGGCTGGGGCTCCAGGACACTGGGACATGATGGGACATGATGGGACATAGCAGAG
 ATAGCACAGCTGTGGGACACTGGGACAGGGGGGACATTGACAGAACAGGAAGGTGACAGAGTGTGCTGGGGACTCAGAGTCCCGAGGGGA
 GGTGTCCCTGGTGACCTCATGGCATCCTCAG TTC TCA GCC CTG GCC CTG AAG ATG GGG ATC CTC TAC TAT GGG
 F S A L A L A L K M G I L Y Y G
 GGG CAG CTG GTG GCC GCG ACC GTC AGC ACT GGG GAC CTC GTC ACC TTC CTC CTC TAC CAG ATA CAG
 G Q L V A A G T V S T G D L V T F L L Y Q I Q

FIGURE 7 - SUITE 1

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Figure 7

TTC ACT GAT GTC CTG GAG GTGAGCCTGAGAGGATGCCCATATCCGATGTCCCCATGTCTCCCTGCCACAGTCACAGTGTGTCA
 F T D V L E
 CAGTGTCCCTGTGTTCCCTACATCCTCCCTGCTGTGTCTCCAGGGCCAAATCGAGTGTGTCCCCATGCCCATCCATGTCCCTGTGTCCCCACG
 TCTAACCCCTGTGACCCCTGCCACATCCCTGTGTCACTCCTCTGTCTCCCCATACCTACCCCGTCCCTGTCCCTATGCCAATCCCACTGTGT
 CCTCTGGTCCCCATGTCACCATGCCACATGCCCTTGGCCCTCCTGGCCACGTCACTAGCTGTCCCCAG GTC CTG CTC GAC TAC
 V L L D Y
 TTC CCC ACA CTG ATG ANG GCT GTG GGC TCT TCG GAA AAA ATC TTT GAG TTC CTG GAC CGG GAG CCA CAG
 F P T L M K A V G S S E K I F E F L D R E P Q
 GTC TCA CCC TCA GGG ACA ATG GCA ATG GCT GAC GGC CAC CTC CAG GGC CAG CTG GAG GAT GTC TGG TTC
 V S P S G T M A P A D L Q G H L Q L E D V W F
 TCC TAC CCT GGG CGC CAG GAA ACC CGT CCT CAA GTGGGCACAGACACAGCCAGGGGACACGGGGTGTGGTGGGACA
 S Y P G R Q E T R P Q
 GCGTGACAGGTGTGGAGCACAGTGGGTGATTCAGGGACATGGATGTGATGGACAGGGTGTGAGGATATGAAACAGGAGATACATGGAGG
 GGGTGTATGGGACACTGGAGAGGGACATGAGATCATGTTATGAGGGCGGGGACATGSCACATGTGGGTTTGTGSCACTGGGACAT
 GATGAGTGACACAGAGACATGGTGGGAGGGCATGGGAATGTAGAGGCCGTGGTA
 GGG GTA TCA CTG GAG CTG CGC CCC GGG GAG GTG CTG GCA CTG GGA CCC CCG GGC GCA GGG AAG AGC
 G V S L E L R P G E V L A L L G P P G A G K S
 ACT CTG GTG GCC CTC GTG TCC CGC CTG CAC CAC CCC ACG GGC CGC CTG CTG CTG GAT GGC CAC CCC
 T L V A L V S R L H Q P T A G R L L L D G H P
 CTC CCC GCC TAC CAG CAC TCC TAC CTG TGC CGC CAG GTGAGCAGCCACATGTCCCCATGGCTCCTGTGTGTCCCCCTG
 L P A Y Q H S Y L C R Q

FIGURE 7 - SUITE 2

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TGTCTTGATATCAGCAGCATCTCATTTGATCACCAGATATCTGGGTCCCAGCCATCACCACACACCCCTGATGTCTCTGCCATATCA
 CCACTGTGTCCCTGAGTGTCCCGGCAAGTCCCAACCATCTTGTGTCCCAACCATCCACCATGTCCCCAGATGTCCCTGACACAT
 CCCCAGGCATCCCCACCGCTCCACTGCCACGTTGCCCATGTTCCCGAGTGTCCCGCCCACTGCAG GTG GCC GTG GCC CCG CAG
 V A V V P Q
 GAG CCG CTG CTT TTT GCC CGC TCA CTC CAC GCC AAC ATT TCC TAT GGG TTG GGG GGC TGC AGC CCG GCA
 E P L L F A R S L H A N I S Y G L G G C S R A
 CAG GTG ACA GCG GCC CGC CGG GTG GGC GGC CAC GAC TTC ATC ACT CGC CTG CCC CAA GGC TAC GAC
 Q V T A A A R R V G A H D F I T R L P Q G Y D
 ACA G GTPAAGCTGTCCCTTTCTGTTCGGGTCCCTCCATGTCTCCCTCCAGCCTGACCCCGCTCGTCCCGCAG AG GTG GGC
 T E V G
 GAG TTG GGA GGA CAG CTC TCC GGG GGG CAG CGG CAG GCG GTG GCC ATT GCC CGT GCA CTG CTG CCG GAC
 E L G G Q L S G G Q R Q A V A I A R A L L R D
 CCC CGC ATC CTC ATA CTC GAC GAG CAC ACC AGC GCC CTG GAC AAT GAG AGC CAG CAG CAG GTGGGATGTC
 P R I L I L D E H T S A L D N E S Q Q Q
 CCCCACGTCCCGGTGTCCCAACATCCCCCTGAGCCCTGTCTCCCTCAGATTGCACGCTAGGTCCCGCATGGTCCCGCTGTCTGGTGTCCC
 CTTATCTCCACTCTGGTGTCCCTCGGTCCCTGGCAGTGGGTGAGGAACATCCCCCTGAACCGTTTCTCTCCACAG GTG GAG CAG
 V E Q
 GAG ATC CTC GCA GCC AAA GGG TCG GGG CGT GCA GTG CTG ATG GTG ACG GGG CGG GCA GCC CTG GCG GCG
 E I L A A K G G S G R A V L M V T G R A A L A A

FIGURE 7 - SUITE 3

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Figure 7

CGG GCA CAA CGA GTG GTG GTG TTG GAG GGG GGA GAG GTG CGG CAG GAG GGA CCC CCC CAC GAG GTG GTG
 P A Q R V V V L E G G E V R Q E G P P Q E V V
 CGC CCC GTC AGC CTT NTT GCG GGA CTG GGG ACA ACA AGG GAG CAC CGG GGG AGG GGG ACA GAG GGA TAG
 R P V S L ? A G L G T T R E H R G R G T E G *
 CGGGAGTTTGGATGGGGAGGGGCGGGGTGGGTGGGATGGGGACACTGCCGTTGGGGACACTGAGGGTGGAGGTGGGGACAC
 CGGGGACGACACAAAGGACCAAGAGCTGTGCCGTGGGCACATGGATGCCGAGCCGGCGGCTGCCGTGCCGTGTACGACACACA
 ACGGCCACAGCATGGACTGCAGTGCCACTGAGTGCCACCAGGGCCGGGGTGGGACACAGAACTGGGAATAAGCCCGCATGTTGT

FIGURE 7 - SUITE 4

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Figure 8

TAP2G

-213
 CGCCATACATTTTGGCCCTGTTCATGCACGGTGNATATGGCCGACCTGGCCNTCATGTGGCCCTGGCCCANTTCTTCCAGCACTGGCCCA
 TTGGGCTGGTGGC -107
 -106
 TCCTGGGGAGGCCGGGCTCGCCCTCTCTGGTGGTGGGGGGGGGGGGGAGCTGCTGGCCCCCAGGGACCCCGTGGGGCTGCAGTGTCTGCT
 AGCATGGCCCCGCC 0
 +1 ATCTTCTGACCTACGGGGCTATGTAGTCTGCTGGAGTCCCGGTGCTGTGSCC ATG GCA ACG CCG TC
 TGG CTG GTG CTG ACC CAC +93 5'UT
 W L V L T H M A T P S
 +94 GGG ACA GCT GTG GTG GCA TTG CTC ACC TGG AGC CTC CTG GTC CCC ACT GTG GCC ACT GGG
 GCA AAG GAG GCA AAG GCC TGG +174
 G T A V A L L T W S L L V P T V A T G
 A K E A K A W
 +175 GTG CCC CTG AGG CGG CTG CTG GCG CTC GCG TGG CCC GAG TGG CCG TTC CTT GGC TGT GCC
 TTC CTC TTC CTC GCA TTG GCT +255
 V P L R R L L A L A W P E W P F L G C A
 F L F L A L A
 +256 GCA CTG GGT GAG ACC TCA TTG CCC TAC TGC ACC GGG AGG GCT GTG GAT GTC CTC CGC CAG
 GGG GAC GGC CTC GCC GCC TTC +336
 A L G E T S L P Y C T G R A V D V L R Q
 G D G L A A F
 +337 ACC GCT GCT GTC GGC CTC ATG TGC CTG GCC TCT GCC AGC AG
 GTAGGACCCCATCCCTCCACAAACCCCATCCACCTCTGGTGGTGTCT +429
 T A A V G L M C L A S A S S

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+430
GGTGGGTTGGGGTCTCTGTCCATATCTGGGGGTCTATCTGATGGGTTCTGGGCACCTCCACTGACCCCTTTGTGATGTCTGAAGGGTTCTG
GCTCTCCATTGACCC +536

+537 CTGATGGGTTTGGAGTCGGCCCCCCCCCAATTCCTTCCAG C TCG CTG TTT GCC GGC TGC CGC GGT GGC CT
TTC ACC TTC ATC AGG TTC +624
S L F A G C R G G L

+625 CGC TTC GTC TTG CGC ACC CGC GAC CAG CTC TTC TCC AGC CTG GTG TAC CGG GAC CTC GCC
TTC TTC CAG AAC ACC ACA GCA +705
R F V L R T R D Q L F S S L V Y R D L A
F F Q N T T A

+706 G GTACAGACTGGGGGCACCTTTTGTCCCTGTCCCCACACCATACCCCCAGCTCACCGTACTCAACTCCACAG CT GAG
TTG GCC TCC CGG CTG ACC ACC +828
L A S R L T T A E

+829 GAT GTG ACG CTG GCG AGC AAC GTG TTG GCA CTC AAT ATC AAC GTC ATG CTG AGG AAC CTG
GGG CAG GTG CTG GGG CTC TGC +909
D V T L A S N V L A L N I N V M L R N L
G Q V L G L C

+910 GCC TTC ATG CTG GGG CTG TCC CGG CGC CTG ACA ATG CTG GCA CTG CTC GAA GTG CCG CTC
GCC GTC ACC GCA CGG AAA GTC +990
A F M L G L S P R L T M L A L L E V P L
A V T A R K V

FIGURE 8 - SUITE 1

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Figure 8

+991 TAT GAC ACC CGG CAC CAG
GTGATAGCAGGGATGGATGGTGGGTGACAGGGATGGAGGCAATGGCAATGGGATGGGAACAGTGGGAGTGGGGAT +1091
Y D T R H Q

+1092
AGTGAGGTGGGATTTGTGGGTGACGGGTGGCAGGGATGAGGGCAGCTGCAATGGGATGGGACAGTGGGAATGGGGAGAGCAGGATGGGGA
CATGGGTCCACACA +1198

+1199
GCAAGGATGAGAGGATGGAGAAGAGTGGAGCAGGAGTGAAGTGGGATGGCGAGTACTTGGCCATCCCATGGGTGCTGACACCCACTGTCC
CCCCAG ATG CTG +1302

M L

+1303 CAG CGG GCC GTG CTG GAT GCA GCA GCC GAC ACC GGA GCG GCA GTG CAG GAG TCC ATC TCT
TCC ATT GAG ATG GTA CGG GTC +1383
Q R A V L D A A A D T G A A V Q E S I S
S I E T V R V

+1384 TTC AAT GGC GAG GAG GAG GAG GAG CAC CGC TAC AGC CAG GTG CTG GAC AGG ACC CTA CGG
CTG CGG GAC CAG CGG GAC ACA +1464
F N G E E E E H R Y S Q V L D R T L R
L R D Q R D T

+1465 GAG AGG GCC ATT TTT CTC CTC ATC CAG CGG
GTGAGGCTGACACAGGGGACACCCCTGTGTTCTGGTGGGATCGGACATCCCGCTGAGGCCAT +1561
E R A I F L L I Q R

+1561 CCCCACAG GTG CTG CAG TTG GCT GTG CAG GCA CTG GTG CTA TAC TGT GGG CAC CAG CAG CTC
CGC GAA GGG ACC CTC ACT +1641
V L Q L A V Q A L V L Y C G H Q Q L
R E G D L T

FIGURE 8 - SUITE 2

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+1642 GCC GGC AGC CTC GTC GCC TTC ATC CTC TAC CAG ACT AAA GGT GGC AGC TGC GTG CAG
 GTGAGGTCAGGCGTGGTCTGTCACCG +1729
 A G S L V A F I L Y Q T K A G S C V Q

+1730
 GATCCCCATGACTGTGGCCACATCCCCGTGTCACCCCTGGGTGCTGTGCTGGGGTCAATCCCCATGTCCTATCCTGGGTGCTGTG
 CATGCAG GCA CTG +1834

A L

+1835 GCG TAC TCC TAT GGT GAC CTT CTG AGC AAT GCA GTG GCC GGC TGC AAG GTC TTT GAT TAC
 CTG GAC TGG GAG CGA CCT GTG +1915
 A Y S Y G D L L S N A V A A C K V F D Y
 L D W E R P V

+1916 GGT GCT GGT GGC ACC TAT GTG CCC ACC AGA CTG CGG GGC CAC ATC ACC TTC CAT CGG GTG
 TCC TTC GCC TAT CCC ACT CGC +1996
 G A G G T Y V P T R L R G H I T F H R V
 S F A Y P T R

+1997 CCT GAG CGC CTC GTC CTG CAA GAT GTC ACC TTC GAG CTG CGC CCC AGT GAG GTG ACG GCG
 TTG GCG GGG CTG AAT GGC AGC +2077
 P E R L V L Q D V T F G L R P S E V T A
 L A G L N G S

+2078 GGG AAG AGC ACC TGC GTG GCA CTG CTG GAG AGA TTC TAT GAA CCT GGG GCC GGG GAA GTG
 CTG CTG GAC GGG GTG CCG CTG +2158
 G K S T C V A L L E R F Y G P G A G E V
 L L D G V P L

FIGURE 8 - SUITE 3

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Figure 8

+2159 CGG GAC TAC GAG CAT CGC TAC CTG CAC CGC CAG
 GTGANZGGGTGGGGGAATGTTAGCTGCACTGAACANTGCTGGGGCTGACCTCTGCCCTGG +2254
 R D Y E H R Y L H R Q
 +2255 GGCAG GTG GCA CTG GTG GGG CAG GAA CCC GTG CTC TTC TCT GGC TCC ATT CGG GAT AAC
 ATT GCC TAC GGG ATG GAG GAC +2335
 V A L V G Q E P V L F S G S I R D N
 A Y G M E D
 +2336 TGC GAA GAG GAG ATC ATA GCA GCT GCA AGG GCT GCG GGT GCT TTG GGC TTC ATC TCT
 GCA CTG GAG CAA GGC TTT GGC +2416
 C E E E I I A A A R A A G A L G F I S
 A L E Q G F G
 +2417 ACT G GTGAGTGTGGGAGCAAGGGGGGACCCGGGTGTCTGACCCCACTCATCCCACTCATCCTGCAG AC ---
 GTA GGG GAG AGA GGG GGG CAG +2511
 T
 G E R G G Q D
 +2512 CTG TCA GCG GGG CAG AAG CAG CGC ATC GCC ATC GCC GGT TTG GTG CGG CGT CCC ACC
 ATC CTT ATC CTC GAC GAA GCC +2592
 L S A G Q K Q R I A I A R A L V R R P T
 I L I L D E A
 +2593 ACC AGT GCT CTG GAT GGG GAC AGC GAT GCA ATG
 GTGAGCACTGAGCAGTGGGTGGGGAGGGTCTG?CCCTGCAGTGCATGCTGATGGGAGCTG +2688
 T S A L D G D S D A M
 +2689 TGTCTCCTACAG CTA CAG CAG TGG GTG AGG AAC GGA GGG GAC CGG ACG GTG TTG TTT ATC ACC
 CAC CAA CCA CGG ATG CTG +2769
 L Q Q W V R N G G D R T V L F I T
 H Q P R M L

FIGURE 8 - SUITE 4

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+2770 GAG AAG GCA GAC CGC ATT GTG GTG CTG GAG CAT GGC ACG GTG GCT GAG ATG GGG ACA CCC
GCC GAG CTG AGG ACC CGC GGC +2850
      E K A D R I V V L E H G T V A E M G T P
A E L R T R G

+2851 GGA CCC TAC AGC CGG CTG TTA CAG CAC TGA
GAACCATGGAGCAGCTGGAGTGGCATGGCATGGGATATGGGGAGCAGTGAAGTGGCTTTGCTTCCAGC +2947
      G P Y S R L L Q H *

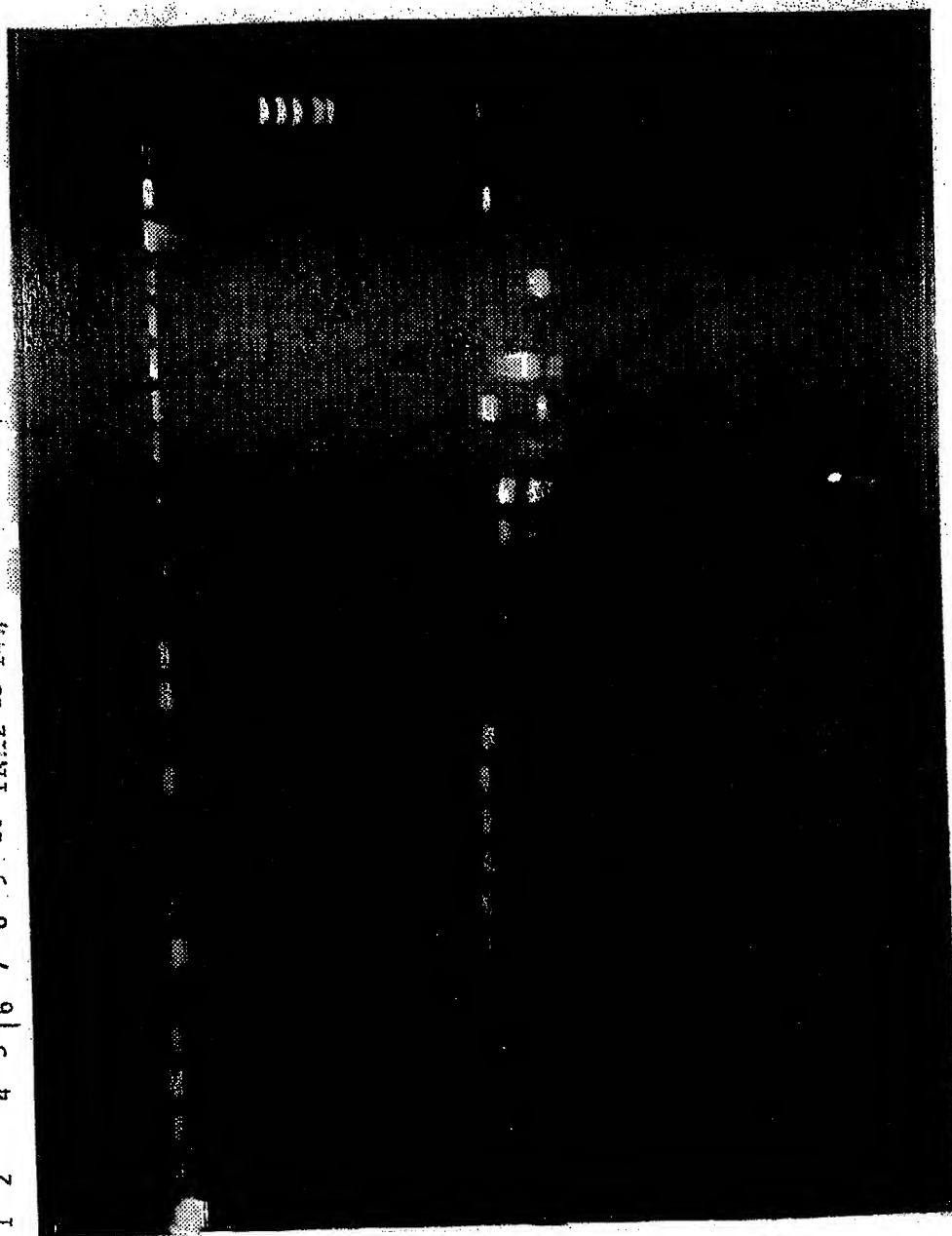
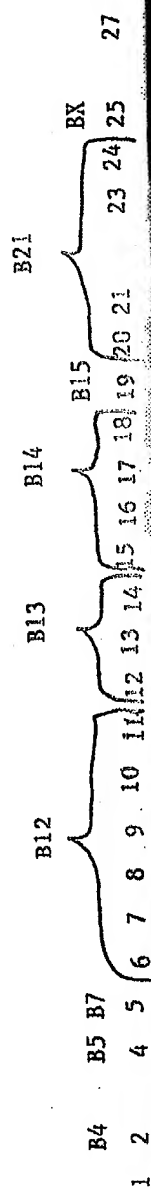
+2948 TGCAGGATGGGATGTTTGGGATTGTGTGGATATAAAGTGGAGATGCTTTTGT
+2999      3'UT

```

INTRON 2-3 : EF23(1B-1R)3R
 INTRON 3-4 : EF23 2(1)
 INTRON 4-5 : EF23 352H CON
 INTRON 5-6 : EF23224RS
 INTRON 6-7 : EF23(5B-5R)1R
 INTRON 8-9 : EF23277B CON
 INTRON 9-10: EF23 43RSR
 INTRON 10-11: EF23 43RSR
 INTRONS 1-2 ET 7-8 INEXISTANTS CHEZ LE POUET

FIGURE 8 - SUITE 5

FIGURE 9



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A5FIN.txt

GTCCCTATTCCCATTGTGTCTCCTCACATCTGCCATCTCTTCTGTCCCCAT
CTATGCTTTGTGCCCCCATCCCTTACCCCATCCCCACGTGTCCCTGTGG
TGCCACCTCCACACGTGTCCCGTGTCCCCACAGCGGGGCGGTGGCGCAA
TAACACTGTGATGTGGCGCTGTGCCGGGACGGAGCGACGGCGCTGCCCA
TCCGTGCCACGTGCCAGCAGAGGGGACAGCGGGTGACGACGGCCGGGGGC
TGCCGAGACGCCTTCTGCACTGTGTGAGGTGGCACAGAATCTGCGGCG
GAAGGGACAGCGCGGGGGGTGGCACGGGTGAGTGTGAGCAGTGTCCCC
ATAGAAATGGGGACCCATTGGTGTGGGGAGGTTTGGATAAGGGGTCCCC
ATGGGTGGTGGCACATGGGGACATCCCATAGCCTGGGATCCCATGGTTGG
GGCCATCCCGTACCTGGGATCCCCACATGGGAGGATGTCCCCCGCTGTCC
CCATGGCAGTGATGGAGGCACAGCTGGCAGAGCAGCTGTTGGATGATGAT
GAGGACGTCCCCACGAGGAGCTTCTTCCCTGAGAGCTGGCTGTGGCGACG
CATCCATGTTGCTGGCACTGCACGGTGTGTCCCCGTGTGTCCCCATGTCC
CCATGTCCCCATGACTTTGTGTCCCCGTGTCCCCATCTCCCCATCTCCCC
AGGCTCTCAGTGTCTCCCTGACTCCATCACTACGTGGGAGATTGAGGC
AGTCGCCATCGTCCCTGGACATGGTGAGTGTACCCCCCTCCAATGGCCCT
GCAGTGTCCCCCTGACATCCCCCTCGTGGTGTCCCCATGTCCCCCACGTC
CCCAAGTTCTATGGTGTCCCCATGTCCCCCTCTCCCCCTCCCCCGGA
ATGTCCCTGTGTCCCCGTGGTGTCCCTGCACTGCCCCGCACTGATGAGGT
CCTGGCAGGGCTGTGCGTGGCGGAGCCGACGGGTGACGGTGACACAGG
ACGTGCGTGTGGCGCTTTGGCTGCCCCCAGCATCCGGCCCTAGAGCAG
ATGCAGCTGCAGCCTCATCCACAGCAGACTGCCCCGACGATCAACGT
AAGCCCTATAGAGACCCCATAGGCACCCAGAGATACCTCTTTCCCTCTA
ATAAATAACCACTTTGCTTCCAATAGATAACCCTCCTGCCCCATAGGTACC
CCTGTGCTCCATACTTGCCCTGCCACAGCATAACATACCCCTTTCCCTCCA
ACAGATATGCGTTGCCCCATAGATACCTTCTTTCTGCCCTATAGATAACC
CCTCATGCCCCACAGATTCCCGTTTCTTTCAATTGGTACCCCTGCCCC
TCATATATCCCCCTTACCCACGGATACCCCTTAGACACCCGGTACCA
CTTCTGCCCCATGGATACCCCTGTGGCACATAGATAACCGCTTCTGCCCC
ACAGATACCCCTTCTACTCCACTGTCCCACAGCCCCACTGCCCCATG
GCCACCCATAGCCTGGTGGCATCGGGTGACAGTGACGGTGATGCAGGTGA
CGGTGACACTGTGCGCAGTGGAGGGGGTGTGCGCGGCGCTGGATGGGGTC
CCCCAGATGCTGGAGCTGCCCCGGGGAGGGCAGTGGCTGCACCCCTCAC
TCTGGTGGCCCTCCACCCTGGGGACATCCCATCACCATCACCAGCCCGCG
GGCCATGGGGGCTGGGGGACCGTGTACCCGAGTCCCTGCATGTCGAGGTG
AGATCAGTGGGGTCCCTCCAGTCACCTGGGTACCTCTGGGGTCCCTTA
AAGCCCTGCGACCTCCTGGACATTGTTGTCTTGTGAGCCTGCGGTACCC
CTGAATACTGGGGCTGTCACTTTGAGGTTTATGGACACCATGTCCCTGTG
TCCATGGTGGCCCTGGACATGTTGGTCTTATGGGATCTGGGGACATGGG
GTCTTGGTGGTCTGGATACTGCAGTTGTCTTTTGTGGACACTATGTC
CCCATGTCTTGGTGGGAATGGTGTGATCCATTCCCGCAGCTGAGGGAG
AGCTGCACCTGGAGGAGAGCACCTACATCCTGGACGCAGATGGTGGGTGT
GAGGACTGGGGGACACTGGGGAACTGGGGACGTGGGGCCGGACCCTGTG
GTGTGGTGTCCCTACAGATAAGCGGAGCCGGAGCCTGAAGCTGCCGGGGG
ACGTCCCTGCAGAGATCGTCCCTGATGGGGACTTCAGCATGAGCATCCGT
GTCAGTGGTGTGTGGGGATGGGGACATGGGGTGGGGACATGGGGGTGGGT
ACTGGGAACGTGGTGGGGATGTGGTGGTGGGCATAGGGGACATGGGGACA
TGGGAGGACATTTGTTGGGGACATTGATGTCCATCCCTGATCATCTCTCT
GTCCCTATGTCCCCATACCCATGTGTGTGGCCATGTCCGCACGCTGTGCC
CCTGTGTGTGTCCCCCTGGGTGTCCCCACATGTGCTCACATCCTTATTACA
TCCCCACATCTCTG. GTACAACCCCGTGTGCCCTGATGTGTGCCCTCC
ACACATCCCCATGGGTGTCCCAATGTTCCCATGTCCCTCTGCTCATCCCC
ATCCACATCCCCATGCCCTATGCCCTATGCGGAGCTTCCCGGCACTTTTCCA
TCTTATCCCCATGTCCCCATGTCCCATATCTCCATACCCCTGTGACCCCA

FIGURE 10

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..5FIN.txt

TATCCCTGTCCTTCAACTCCCCTCCCATCCCCACACCATCCCCATGTCTT
CTGTCCCCACACCATCCCCATATCCCCCTGTCCCCCTGTCCCTGTCCCA
GGCCGGGTGCCGGGCTGGGCACTGCAGGGCGCTCTGGGGATAGGGGACTC
TCTGCTCCGCTCCCCCGGGGCTGTGGGGAGCAGTCCCTGATGTCAATGG
CACCCACTGCTGCTGCTCTGCGCTTCTGGATGAGAGCGAAGGGTGGGGG
CAGCTGCCCCCAGGGCACCACAGCGCGGCCTCAGAACCCTGCAGCAGGG
TGAGCTATGGGGCAGGTTGTGCTTTATGGGGTGGGCAATGCTTTATGGGG
TGTGCAGTGCTCCAAGGGATGTGCAGTGCTTCATGGGGGATGCAGTGGGG
TTTGATTTGATTTGATTTATGGGTTTGCAATTTCTCCTCCGAGGATTGCAT
CTCTCTATGGTGTTTGCAATGGGATGTGCAGTGCTCCAGGTGGAGGTGCA
GAGCCCTATGGGGGTGCAGTGCTGTGTAGGGGATGTCTGTGGTGTCCTCA
ATGGTCTCTGATGTCCCCACAGGCTTCGAACGGGTGCAGAGCTTCCGCAA
AAGTGACGGCTCCTATGGGGCATGGCTGCACCGGGACAGCAGCACCTGGT
GAGGGGAGCGGGGATGATGTGGGGACATGGGGATAGTGAGGGGATGTGGG
GATGCTGGGGTATGGGGATGTGAGGACATCATAGGGACATGAGCGGTGGG
GCCATGTGGATTTGGGGACGTGGTGACACGGTGCTCCTGGTGCAGGCTGAC
GGCACTGGTGCTGCGTGCTGGCCCTGTCCCGGCCCTATTTGCCAGTGG
CTGCCAGCGGCCCGCTGCGTCCCTGCGGTGGGTGCTGGGGCAGCAGCGC
CCAGATGGCGCCTTCTTGGAGCACAGGGCTGTGGTGCACCGTGAGATGCA
GGTGGGTGACACATCACTGCTGTGTGCAATGTCCCCATGCAGGATCTCCC
CCTGCAATGTCCCCTGAAGGTCCCTGCAGGCTGACCCACATTACACTGT
GTCACTCACGTGTCCCGTGTCCCCAGGGTGGTGTTGGCAGACCCCGGCC
GGAGGCCACCGTGTGCTGACGGCCTTCGTGGTGGTGGCCCTCCATGGTG
CCCGCGCTCTGCTGCCCCCGGACAGCCCTGAGCTGCCCTCCTGGTGAGT
CCCATGTCCCCACCCCTGTGTCTTGGTCTCATATCCATGTGTCCCTGT
GCCCCATCCCCAAATCCCCACATCCCCCATATGTTCCCATACCCCTGCTG
TGTCCCCCAGTGTCCCCCGTCTTTTCATTCTCCACTATCCCCCGTATTC
CCATATGTCCCCCTGTCCACAGTGTCCTCATCCCTCTGTGTCCCCCT
GTCCCCCAGTGTCCTCCAGTATCCCCATGCCTCCCCGTGTCTCTTCA
CCCCATGTCCGTGTCTCCAGTATCCCCATGCCTCCCCGTGTCTCTTCA
TGCCCCCACTCCACGTCCCCCACTCCATGTCCCACTGCCACAGGACAA
ATCCCTGTCCCGGGCCTCCACGTTCCTCCGGGGCCGCTGGAGCAGTTGG
GGACCTATGGGACAGCCATTACATCCTATGCATTGGCACTGGTGGACACC
GCTCCTCCGGGGCCGATCCGCGGTGGAACGTCTGCGGGGCATGGCCCCG
GAGCGGCCACGGTGCGTCTGTCTGTCCCCATGGGGTGGTGGCACCTCT
GTCCCCATGGCTGCCTCCTGGACCCCTCTGTCCCCTCCTTCAGATTCAT
CTCATTCGAATCCTTCAATTTTATTCTCCCTCAAACCTCTTCTTTGTA
TTCTTCACATTCATTCTATTCAAATTGCTCTCCTTCTGTCTGTCTTC
TTCAAATCTTCTTCAATTTTGTCTCCTGATTAATTCTCTTAAATTA
CTCTCGATCAAGTTCTGCAGATTCGTTCCACTTCGGATGGATTCTTCTCC
AAACTGTTCTTCAGATTCATCTCCTTCAATTTCTTCTTCAATTAATT
CTTCTTCAGAGTGATTCTTCAAACCTCTTCTTCATGTTCTCTTCAAGTCCA
TTCCCTGCACTGACTCCGGGTGCTCAGGACCCCCCGTGACCCCATATGA
CCCCATATGAACCCCCCATGACCTCCACAAAACCATATGACCCCGTGACC
TCCCATGACCCCTCATGACCCCATATGACCCCATGACCCCATCCCTGT
GCAGGTGGCCGTGCAACCTTCTGGCCATCCGGTGGCCCCGCAGCCACGGT
GGAGGCGACGGGTTACGCCCTTCTGGCACTGCTGCAGAGCCGCGACATCG
CCGGGGCTGCGAGGGCGGCACGGTGGCTCCGACAGCAGAGCAATTACGGG
GGTGGCTTCCACTCCACGCAGGTGGGTGGGGGTCACTGACCCCGGGTG
CCTCGGGGTGGGGGTGATTTGATCCCCAGGTACCTCTTGGTGGCTGTGT
CCCCAACCTGCTTGGTGTTCCCGCAGGACACGCTGGTGGCCCTGGAGGCG
CTGGCCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGGGCTGAA
CCTGGGGCTCTCCTGGCCGGGGGTGCCCGGGGGAGGGCTGGTGGCACTC
AGGTTATGCTGAAGCCGGGGCTGGAGCCGCTGGAGCAGGAGCTGCAGCTG
GGGACATGGCGGGATGTGGGGACACGAGGGATGTGAGGACATGGGGACA

FIGURE 10

SUITE 1

TGCTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATGGTAGGA
CATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGACATGATG
GACACAGGGCTTTGGGGTCCTTGGGGTCCTCGCTCTGTCCCCATGTCCCCA
GGTGCCTCTGGGCAGCCAGTGACAGTGCAGGTGGAGGGACACGGCGAAG
GGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCCAAGACC
GATGTCCCTCACAACTCCCTCATGGTGTCCCTCATGCTGCCACGGT
GTCCCTGCTGTCCCATCATGGTGTACGCTGTCCCCAGGTGCTCCGCCA
GTTCCGCTGCTGTACCTCCGAACGCCACGTGCCAGGCGCTGCACCTGG
AGGTGGCCATCACCGGCCCATCCTGTACCATGGTGAGGCCCCACCCAAA
GGCCCCGCCCTTTTCTCGGGGGGGCGTGCCCTCAACCCTGTTTTGC
ATATCCCAACCCCCAGCAGATGAGGACTACGAGGACTACGAGGACTACGA
GGAGGCGGAGCCTAAGGAGGGGGAGGAGCCTACGGAAGGGGAGTGCCCG
TGGAAGGGGCGGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCC
TTATGGGATGCCCGTAAGCGGCAACGCCGACGACACATAACCCTGCCCA
CGAGGTGGCTTCTGCTGTCTCCGGTGAGGGGCGGAACCTTCTGTCC
CTGGGGGCGGGTCTTCTGCTGATGGGCGTGGCTTATTGCTGAGGGGCGT
GGCCTGTTGTAGGCGGAGCCCAGGGGTGGCACTGACTGGGATGGCGGTGG
TGGAGATCACTCTGCTCAGTGGCTTCTCACCCCATAGAGCTGACCTGGAC
AAGGTAGGGGCCCAGGGGGACTTGTGGGACATGTTGGGGGGTTGAGGGGA
GTTATGGGGTGTGGGGTTTGGGGGTGTTGGAGTTGTTGAGGTGGCAGAAT
GTTTGGGTTGGAGTCATGGGATATGGGGCTATTGGGGTTTGGGGTGTG
TGATGTTGGGAAACATTGAATTGGGGTTGTTGAGTTTGGGGTGTGGGG
TGTGCGGGTGACAGCTGCAGCTGCTGGGTGGAGTATTAAGGTGTTGGG
ATGTTGGGGTGTGGATGGCTTGGATGCGGGTGTGGGGTGGGCACGTAT
CTGGGTGCTGCTGTCCCAACAGCTGCGGGACGTGGTGGATCACTGGAT
CAGTCACTATGAGTTGGAAGGAAACAGTTGGTGTCTATACCTGGATGAGG
TGTGTCTCCCGTGTACCCCTATAACCCAGTGGCCCCATGTTCTCATAT
CCCCCATGTCCCGTGTCCCAACCATATCCATTCTCCCCACACATCC
CCGTGTTCCACCAGCTGTCTCATTCTGTCCCTGTCCCCAGGTCCCCC
CGAGCGGCTGCAGAGCTGCAGCTGCTGGGTGGAGTATTAAGGTGTTGGG
ACATGCAGCCGGCAATGGCAGCCATCTATGACTACTATGAGCCTGGTGGG
TGGGGCCTTCAGTGGGAGGGGCTAAATGGGTGGTGGTCTTCATGGGTGT
GACCATTTGGAGGAGGCGTGGCCGATCTGACCCCTCCATGCCCCATCCAGG
ACAGCGCTGCACCGTCTTCTACAACGCCCCCAAAGGAGCAGCACCATCG
CCACACTGTGCTCCCCAAAATCTGTGAATGCGCCCAAGGTAGGACCCCA
CTGTGACTCCATATGTAGGGCCCCCATCCAGTGAACCCCAACATCCTCCT
CCTAATTTTGAAGATCTGGGGGTGAAATTATGGGGTTTATAGGGGAGCG
TGGTTGAGTGACATGCAGGACATGGAGGGAACCCACACCAAGAACCTTGT
GTTTTGGGTCCCTGATGATGTTGGGAGATCCTATTGATGTTGGTGGTCCC
CAGGGGGGTGTCCCCAAGCCCAAGGAGGACACAGGAGGTGACAGCTGAT
GACCGCCATGACTTTGCCTGCTACAGCCCCCGCGTGGACTATGGTGGAT
CCCAAATCACTGCACCTCAAACCTGACCCCAAATTGGCTGCATCCCGAAC
CCCAACTGCCCTAAATCCCATCTGCTGCCCTGAGTCCCACAGCTGCACA
CTGTACCCACAACTGGCCCCCTGAAGCCTAAAAACATTACGAGGATTTT
GTAGTTTTCTCCCTGTACCCAGTTGTCCCTCTGACCCCAAGAACCCAC
AGCTGCCCTATGCTGTCCCTGCCCCGCCATAACTCCTCTGATACAATAAC
CCCCGTGACCCCATCTTTATGACCTCCATGACCTTTGACCCCAAGCACTG
GTGGTTGGGGTGTGCTGTCCAGAGTGAGATAGGGGCTTTTGTGGCGTTTGA
GACGGAATCAAGGAGGTGCTGCTTGAAGGTGAGACTGAGGGTAGTGGGA
CGGACTGGAAGGTGAGAATGGGAGCACTGGGAGAGGAGGAGTACTGAG
AGGGACTGGGAATGACTGGAAATTGAGACTGGGTGGACTGGGAACCTCTGG
TAGAGACTGAATGGGTATACTGGGAACACTGGAAGAAGTTGTGGGATGAG
AAGAGGATGCTGGGATAGCAGACCCCCCCCTTGTGCTAGGGGGGTCTCT
CAGCCATACTGGCACAATATGAGAGTATACTGGGTGGTACTGGGAAGCT
GGGAGGACTCATACTGTTCTCTACTGCTGACGGCAGGACACAGGAGTGG

FIGURE 10

SUIITE 2

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A5FIN.txt

CCCCTGGGGAGCGGAGGCGGCTGCTGGTGCGGAAGAGCTGCCCACTGCGC
CTGCAACTCCACAACATCTACCTGGTGATGGGGGGCAGCGGGAGGACGCG
GGACCCTGAGGGGGCGGTGAGAAGGGGCTGTGCCCCATGTCCACATGTCCC
TGTGTTCTCATGTTCCCATGTCCCATATCCAGTGTTCTTAACCCCATAT
CCTTGACCTTGAGCCCATACCTGATATCCCTGACCCTGTCCCCATTCTC
AGCCCCCAGTTCCTGCTGGGCCCCCACTCATGGTTGGAGGAGGTGCCATC
CCCTGGACGCTGTAAGGCCACAAGGTTGCGGGGTTACTGCGCCCAACTGC
AGGAGTTCGCGACCCGCTGAGCCAACCTGGGCTGCCAGCTGTGAGCCCT
GGGAGCCACTGGGAGCATGTTGGGTGCAGCTGGGACCATTCTGGGGGTGA
AGTGGTACCCTGTTGGATCAGTTGGGATCAATTGGGAATAAACTAGTGT
TGACTGGGACCGTGTGTGACCAACTGGAAGTGTGTTGGAAGAACTGAG
AGCTGCTGGGGTTGAGTGGGAGCAACTGGAAGTGTGTTGGAACAAACAGG
GGACCAACTGGGATCACACTGTGGTCAGCTGGGATCACACTGGGTCAAAA
AAGATCACAGTGGCCCAATTGGGGTCATACTGGGGTGAGCTGGGATCAGA
ACGAGTTTAATAAACGTACAGTCGTCCGAGCCACCACAGAGTCAGCCCTC
CAGCGGCGCAGAGCGGCGCAGCGCGCACTGGCTGCCCGCGGTAAGCGGAT
GTGACGTCACCTCGCGGCGCGCTATTGGAACCTCCAGCAGCGCCCCGCGGA
GCGCCCCAATGCCGCGGCCCAAACCGCGCAGCCCCCGGCGCGGGGCGCG
CCCCCCCCGCGCGCCCCCGCCACCCCCCGCGCGGCTCGCGGTGAGTG
CAGCCCGTAGGAGTGCGGAGTGTGGGGCGGGGGGGGGGCGTCTGGAGC
GGAGCCTTTATCACCGCTGTTTTCCCGATTTCCTCCGTCCTTTTCGCCCCGT
TTCAGCCCGCCGGTACCGGCCCGGTGAGAGGGCGCTGCGGGAGATCCGCC
GCTATCAGAGCAGCACCGCTCTGCTGCTGCGCCGCCAGCCCTTCGCGCGC
GTGGTAACGGGACTGCCCCGGAACGGGACACCCCCCAACCCCCCAACGG
GACCATCCCCCACGGATGGATCCCCCCCCACACACATCCAACGTGGGAC
CCCCCGCCCCAAAATGAGATCTCAACGTGAGATCTGGGGGCCTCAAAATG
AGACACTCTCCCCCTCCCCCAACGGAACACCCCGAAAAATGGGACCACAC
ATAAAAGTGGGGACTCCCCCTCCTCCCCCCCCGCCCCGTCAAAATGGAACAC
CCCCAACTGGACCTTTCAAAAAATAACATTCCCCCTCCCCCAAAAATGGG
ACTTACCACAAAGTGGGATCTTCCCCCAAATGAACACCCCTCAAAATG
AGACCCCTCGGACCCCCCCCCAACCCCTCTGCACCCATCNGCCGTCTGCA
CGGAAGGGAAAGGCTGTAGGGTACATCTACCCTTATTCTTGGGTTTGTG
TTTTGTTTTGTTGTTATTTAGAAGCAAAACCAAGACAACAAAGCCCAGCC
AATGCCATTTCTGGCAGTGGACGCAGGCGCAGGCGGGTTGGTCACAAAG
CAAGAAGTTGCTGCGGGACTTTGTCTGTTTTGGGGCCGTTCTCGTGAACCT
CTGAGCCATGGATGAGGAAATTAATGCTGATTTAAGGCATCCTACGG
GCAGTTTGCTCCTGCTAAGCGGCAGCGGTAAGGGATGCTCTGTGTGG
TGGGTGCTCACCAGGCTTGGTTTGGGGGCTTGTCTGTTCTCTGAGAAAC
ACCAGCAATGCTGGTTGGGTTCTGGGTCCACCCTGGCTTGTATGGGGGAG
TAAAGGAAGGGGTGGGGGAGAAGGAAGCCTGGGAATGGCCAGAGGTGTGG
TGGTTTT

FIGURE 10

SUITE 3

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A5FINB.txt

GTCCCTATTCCCATTGTGTCTCCTCACATCTGCCATCTCTTCTGTCCCCAT
CTATGCTTTGTGCCCCCATCCCTTACCCCATCCCCACGTGTCCCTGTGG
TGCCACCTCCACACGTGTCCCGTGTCCCCACAGCGGGGCGGTGGCGCAA
TAACACTGTGATGTGGCGCTGTGCCGGGACGGAGCGACGGCGCTGCCCA
TCCGTGCCACGTGCCAGCAGAGGGGACAGCGGGTGACGACGGCCGGGGGC
TGCCGAGACGCCCTTCTGTCAGTGCTGTGAGGTGGCACAGAATCTGCGGCG
GAAGGGACAGCGCGGGGGGTGGCACGGGGTGAGTGTGAGCAGTGTCCCC
AAAGCGGGGAGGGGTGACCTGGGGTGGTGGCGGTGGGGTGTGGGGAGTT
GTAGAAATGGGGACCCCATTTGGTGTGGGGAGGTTTGGATAAGGGGTCCCC
ATGGGTGGTGGCACATGGGGACATCCCATAGCCTGGGATCCCATGGTTGG
GGCCATCCCGTACCTGGGATCCCCACATGGGAGGATGTCCCCCGCTGTCC
CCATGGCAGTGATGGAGGCACAGCTGGCAGAGCAGCTGTTGGATGATGAT
GAGGACGTCCCCACGAGGAGCTTCTTCCCTGAGAGCTGGCTGTGGCGACG
CATCCATGTTGCTGGCACTGCACGGTGTGTCCCCGTGTGTCCCCATGTCC
CCATGTCCCCATGACTTTGTGTCCCCGTGTCCCCATCTCCCCATCTCCCC
AGGCTCTCAGTGCTGCTCCCTGACTCCATCACTACGTGGGAGATTCAGGC
AGTCGCCATCGTCCCTGGACATGGTGAGTGTACCCCCCTCCAATGGCCCT
GCAGTGTCCCCCTGACATCCCCCTCGTGGTGTCCCCATGTCCCCCACGTC
CCCAAGTTCCCTATGGTGTCCCCATGTCCCCCTCTCCCCCTCCCCCGGA
ATGTCCCTGTGTCCCCGTGGTGTCCCTGCACTGCCCCGAGTGATGAGGT
CCTGGCAGGGGTGTGCGTGGCGGAGCCGACGCGGTGACGGTGACACAGG
ACGTGCGTGTGGCGCTTTGGCTGCCCCCAGCATCCGGCCCCCTAGAGCAG
ATGCAGCTGCAGCCCCCTCATCCACAGCAGACTGCCCCGACGATCAACGT
AAGCCCTATAGAGACCCCATAGGCACCCAGAGATACCTCTTTCCCTCTA
ATAAATAACCACTTTGCTTCCAATAGATAACCCCTCTGCCCCATAGGTACC
CCTGTGCTCCATACTTGGCCCTGCCACAGCATAACATACCCCTTTCCCTCCA
ACAGATATGCGTTGCCCCATAGATAACCTTCTTCTGCCCTATAGATAACC
CCTGAGTCCCCACAGATTCCCGTTTCTTTCAATTGGTACCCCTGCCCC
TCATATATCCCCCTTACCCACGGATACCCCTTAGACACCCGGTACCA
CTTCTGCCCCATGGATACCCCTGTGGCACATAGATAACCGCTTCTGCCCC
ACAGATAACCCCTTCCCTACTCCACTGTCCCACAGCCCCCACTGCCCCATG
GCCACCCATAGCCTGGTGGCATCGGGTGACAGTGACGGTGATGCAGGTGA
CGGTGACACTGTGCGCAGTGGAGGGGGTGTGCGCGGCGCTGGATGGGGTC
CCCCAGATGCTGGAGCTGCCCCCGGGGAGGGCAGTGGCTGCACCCCTCAC
TCTGGTGGCCCTCCACCCTGGGGACATCCCCATACCCATACCCGCCCCGCG
GGGACTGGGGGCTGGGGGACCGTGTACCCGAGTCTGTCATGTGAGGTG
AGATCAGTGGGGTCCCCTCCAGTCACTGGGTCACTCTGGGGTCCCTTA
AAGCCCTGCGACCTCCTGGACATTGTTGTCTTGTGAGCCTGCGGTACC
CTGAATACTGGGGCTGTCACTTTGAGGTTTATGGACACCATGTCCCTGTG
TCCATGGTGGCCCTGGACATGTTGGTCTTATGGGATCTGGGGACATGGG
GTCCTTGGTGGTCTGGGATACTGCAGTTGTCTTTTGTGGACACTATGTC
CCCATGTCTTGGTGGGAATGGTGTATCCATTCCCGCAGCCTGAGGGAG
AGCTGCACCTGGAGGAGACCTACATCCTGGACGAGATGGTGGGTGT
GAGGACTGGGGGACACTGGGGAACTGGGGACGTGGGGCCGGACCCTGTG
GTGTGGTGTCCCTACAGATAAGCGGAGCCGAGCCTGAAGCTGCCGGGGG
ACGTCCCTGCAGAGATCGTCCCTGATGGGGACTTCAGCATGAGCATCCGT
GTCAGTGGTGTGTGGGGATGGGGACATGGGGTGGGGACATGGGGGTGGGT
ACTGGGAACGTGGTGGGGATGTGGTGGTGGGCATAGGGGACATGGGGACA
TGGGAGGACATTTGTTGGGGACATTGATGTCCATCCCTGATCATCTCTCT
GTCCCTATGTCCCCATACCCATGTGTGTGGCCATGTCCGCACGCTGTGCC
CCTGTGTGTGTCCCTGGGTGTCCCCACATGTGCTCACATCCTTATTACA
TCCCCACATCTCCTGTGTACAACCCCGTGTGCCCTGATGTGTGCCCTCC
ACACATCCCCATGGGTGTCCCAATGTTCCCATGTCCCTCTGCTCATCCCC
ATCCACATCCCCATGCCATCCCTATCCCGACGTTCCCCCATTTCCCA
TCCTATCCCCATGTCCCCTGCTCCCTATCCCTGCTCCCTGCTCCCTGCTCCCT

FIGURE 10

SUIE 4

FEUILLE DE REMPLACEMENT (REGLE 26)

TATCCCTGTCCTTCAACTCCCCTCCCATCCCCACACCATCCCCATGTCTT
CTGTCCCCACACCATCCCCATATCCCCCTGTCCCCCTGTCCCTGTCCCA
GGCCGGGTGCCGGGCTGGGCACTGCAGGGCGCTCTGGGGATAGGGGACTC
TCTGCTCCGCTCCCCCGGGGCTGTGGGGAGCAGTCCCTGATGTCAATGG
CACCCACTGCTGCTGCTCTGCGCTTCTGGATGAGAGCGAAGGGTGGGGG
CAGCTGCCCCAGGGCACCGACAGCGCGGCCCTCAGAACCCTGCAGCAGGG
TGAGCTATGGGGCAGGTTGTGCTTTATGGGGTGGGCAATGCTTTATGGGG
TGTGCAGTGCTCCAAGGGATGTGCAGTGCTTCATGGGGGATGCAGTGGGG
TTTGATTTGATTTGATTTATGGGTTTGCATTTCTCCTCCGAGGATTGCAT
CTCTCTATGGTGTTCGAATGGGATGTGCAGTGCTCCAGGTGGAGGTGCA
GAGCCCTATGGGGGTGCAGTGCTGTGTAGGGGATGTCTGTGGTGTCCCCA
ATGGTCTCTGATGTCCCCACAGGCTTCGAACGGGTGCAGAGCTTCCGCAA
AAGTGACGGCTCCTATGGGGCATGGCTGCACCGGGACAGCAGCACCTGGT
GAGGGGAGCGGGGATGATGTGGGGACATGGGGATAGTGAGGGGATGTGGG
GATGCTGGGGTATGGGGATGTGAGGACATCATAGGGACATGAGCGGTGGG
GCCATGTGGATTGGGGACGTGGTGACACGGTGCTCCTGGTGCAGGCTGAC
GGCACTGGTGCTGCGTGTGCTGGCCCTGTCCCGGCCCTATTGGCCAGTGG
CTGCCAGCGGGCCCCGCTGCGTCCCTGCGGTGGGTGCTGGGGCAGCAGCGC
CCAGATGGCGCCTTCTTGGAGCACAGGGCTGTGGTGCACCGTGAGATGCA
GGTGGGTGACACATCACTGCTGTGTGCAATGTCCCCATGCAGGATCTCCC
CCTGCAATGTCCCTGAAGTCCCTGCAGGCTGACCCACATTACACTGT
GTCACTCACGTGTCCCGTGTCCCCAGGGTGGTGTGGCAGACCCCGGGCC
GGAGGCCACCGTGTGCGTGCACGGCCTTCGTGGTGGTGGCCCTCCATGGT
CCCGCGCTCTGCTGCCCCCGGACAGCCCTGAGCTGCCCTCCTGGTGAGT
CCCATGTCCCCACCCCTGTGTCTTGGTCTCATATCCATGTGTCCCTTGT
GCCCATCCCCCAAATCCCCACATCCCCCATATGTTCCCATACCCTGCTG
TGTCCCCCAGTGTTCCCCCGTCTTTCATTCTCCACTATCCCCCGTATTC
CCATATGTCCCCCTGTCCACAGTGCTCCCTCATCCCTCTGTGTCCCCCT
GTCCCCCAGTGTTCCCCACGTCCCTGTATGTCCCCATGTCTCCTAGTGT
CCCCATGTCCGTGTCTCCAGTATCCCCATGCCTCCCCGTGTCTTCA
TGCCCCACACTCCACGTCCCCACACTCCATGTCCCACTGCCACAGGACAA
ATCCCTGTCCCGGGCCTCCACGTTCCCTCCGGGGCCGCGTGGAGCAGTTGG
GGACCTATGGGACAGCCATTACATCCTATGCATTGGCACTGGTGGACACC
GCTCCTCCGGGGCCGATCCGGCGGTGGAACGTCTGCGGGGCATGGCCCG
GAGCGCCCACGGTGCGTCTGTCTGTCTGTCCCCATGGGGTGGTGGCACCTCT
GTCCCCATGGCTGCTCCTGGACCCCTCTGTCCCTCCTTCAGATTCACT
CTCATTGCAATCCTTCAATTTTATTCTCCCTCAAATCTTCTTCTTTGTA
TTCTTACATTATTCTTCAATTTTGTCTCTCCTGATTAATTCTCTTAAATTA
TTCTCGATCAAGTTCTGCAGATTGCTTCCACTTCGGATGGATTCTTCTCC
AAACTGTTCTTCAGATTCACTCTCCTTCAATTCGTTCTTGTAAATTAATT
CTTCTTCAGAGTGATTCTTCAAATCTTCTTCATGTTCTCTTCAAGTCCA
TTCCCTGCACTGACTCCGGGTGCTCAGGACCCCCCGTGACCCCATATGA
CCCCATATGAACCCCCCATGACCTCCACAAAACCATATGACCCCGTGACC
TCCCATGACCCCTCATGACCCCATATGACCCCATGACCCCATCCCTGT
GCAGGTGGCCGTGCAACCTTCTGGCCATCCGGTGGCCCCGCGACATCG
CCGGGGCTGCGAGGGCGGCACGGTGGCTCCGACAGCAGAGCAATTACGGG
GGTGGCTTCACTCCACGCAGGTGGGTGGGGTCACTGACCCCGGGTG
CCTCGGGGTGGGGGTGATTTGATCCCAGGTACCTCTTTGGTGGCTGTGT
CCCCAACCTGCTTGGTGTTCGCGCAGGACACGCTGGTGGCCCTGGAGGCG
CTGGCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGGGCTGAA
CCTGGGGCTCTCCTGGCCGGGGGTGCCGGGGGAGGGCTGGTGGCACTC
AGGTTATGCTGAAGCCGGGGCTGGAGCCGTGGAGCAGGAGCTGCAGGTG
GGGACATGGCGGGATCTGGGGACAGGGGATGTGAGGACACTGGGGACA

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUIITE 5

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A5FINB.txt

TGTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATGGTAGGA
CATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGACATGATG
GACACAGGGCTTTGGGGTCTTGGGTCCTCGCTCTGTCCCCATGTCCCCA
GGTGCCTCTGGGCAGCCCAAGTGACAGTGCAGGTGGAGGGACACGCCGAAG
GGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCCAAGACC
GATGTCCCCCTCACAACCTCCCCCTCATGGTGTCCCCCTCATGCTGCCACGGT
GTCCCCCTGCTGTCCCATCATGGTGTACGCTGTCCCCAGGTGCTCCGCCA
GTTCCGCCTGCTGTACCTCCGAACGCCACGTGCCAGGCGCTGCACCTGG
AGGTGGCCATCACCGGCCCCATCCTGTACCATGGTGAGGCCCCACCCAAA
GGCCCCGCCCCCTTTTCTCGCGGGGGCGTGCCCTCAACCCTGTTTTGC
ATATCCCCAACCCCAAGCAGATGAGGACTACGAGGACTACGAGGACTACGA
GGAGGCGGAGCCTAAGGAGGGGGAGGAGCCTACGGAAGGGGCGAGTGGCCG
TGGAAGGGGGCGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCC
TTATGGGATGCCCGTAAGCGGCAACGCCGACACACATAACCCTGCCCA
CGAGGTGGCCTTCTGGTCTGCTTCCGGTGAGGGGCGGAACCTTCTGTCC
CTGGGGGCGGGTCTTCTGCTGATGGGCGTGGCTTATTGCTGAGGGGCGT
GGCTGTGTAGGCGGAGCCCAGGGGTGGCACTGACTGGGATGGCGGTGG
TGGAGATCACTCTGCTCAGTGGCTTCTCACCCCATAGAGCTGACCTGGAC
AAGGTAGGGGGCCAGGGGGACTTGTGGGACATGTTGGGGGGTTGAGGGGA
GTTATGGGGTGTGGGGTTTGGGGGTGTTGGAGTTGTTGAGGTGGCAGAAT
GTTTGGGTGGAGTCATGGGATATGGGGCTATTGGGGTTTGAGGGTGTG
TGATGTTGGGAAACATTGAATTGGGGTTGTTGAGTTTGAGGGTGTGGGG
TGTGCGGGTGACAGAGCTGCAGCTGCTGGGTGGAGTATTAAGGTGTTGGG
ATGTTGGGGTGTGGATGGCTTGGATGCGGGTGTGGGGTGGGCACGTAT
CTGGGTGCTGCTGTCCACAACAGCTGCGGGACGTGGTGGATCACTGGAT
CAGTCACTATGAGTTGGAAGGAAACAGTTGGTGTCTATACCTGGATGAGG
TGTGTCCTCCCGTGTCAACCTATAACCCAGTGGCCCCATGTTCTCATAT
CCCCCATGTCCCCGTGTCCCCACACCATATCCATTCTCCCCACACATCC
CCGTGTTCCACCACGTGTCTCATTCTGTCCCTGTCCCCAGGTCCCCC
CGAGCGGCAGTGTCTCAGTTTGGGGCCACCCAGGACGCGGCTGTGGGT
ACATGCAGCCGGCAATGGCAGCCATCTATGACTACTATGAGCCTGGTGGG
TGGGGCCTTCAGTGGGAGGGGCTAAATGGGTGGTGGTCTTCATGGGTGT
GACCATGGGAGGAGCGTGGCCGATCTGACCCCTCCATGCCCATCCAGG
ACAGCGCTGCACCGTCTTCTACAACGCCCCCAAAGGAGCAGCACCATCG
CCACACTGTGCTCCCCAAAATCTGTGAATGCGCCCAAGGTAGGACCCCA
CTGTGACTCCATATGTAGGGCCCCCATCCAGTGAACCCCAACATCCTCCT
CCTAATTTTTGAAGATCTGGGGGTGAAATTATGGGGTTTATAGGGGAGCG
TGTTTGAAGTGCATGCAGGACATGGAGGGAACCCACACCAAGAACCTTGT
GTTTTGGGTCCCTGATGATGTTGGGAGATCCTATTGATGTTGGTGGTCCC
CAGGGGGGTGTCCCCAAGCCCAAGGAGGACACAGGAGGTGACAGCTGAT
GACCGCCATGACTTTGCCTGCTACAGCCCCCGCTGGACTATGGTGAGAT
CCCAAATCACTGCACCTCAAACCTGACCCCAAATTGGCTGCATCCCGAAC
CCCAACTGCCCTAAATCCCATCTGCTGCCCCCTGAGTCCCACAGCTGCACA
CTGTACCCCAACAAGTGGCCCCCTGAAGCCTAAAACATTACAGGAGTTTT
GTAGTTTTCTCCCTGTACCCCAAGTTGTCCCTCTGACCCCAAGAACCCAC
AGCTGCCCTATGCTGTCCCCTGCCCCCATACTCCTCTGATACAATAAC
CCCCGTGACCCCATCTTTATGACCTCCATGACCTTTGACCCCAAGCACTG
GTGGTTCGGGTGCTGCCAGAGTGAGATAGGGGCTTTTGTGGCGTTTGA
GACGGAAATCAAGGAGGTGCTTGAAGGTGAGACTGAGGGTAGTGGGA
CGGACTGGAAGGTGAGAATGGGAGCACTGGGAGAGGCAGGGAGTACTGAG
AGGGACTGGAATGACTGGAATTTGAGACTGGGTGGACTGGGAACCTCTGG
TAGAGACTGAATGGGTATACTGGGAACACTGGAAGAAGTTGTGGGATGAG
AAGAGGATGCTGGGATAGGAGACCCCCCTTGTGCTAGGGGGGTCTCT
CAGCCATACTGGCACAATATGAGAGTATACTGGGTGGTACTGGGAAAGCT
GGGAGGACTCATACTGGT

FIGURE 10

SUITE 6

44/110

A5FINB.txt

CCCCCTGGGGAGCGGAGGCGGCTGCTGGTGCGGAAGAGCTGCCCACTGCGC
CTGCAACTCCACAACATCTACCTGGTGATGGGGGGCAGCGGGAGGACGCG
GGACCCTGAGGGGCGGTGAGAAGGGGCTGTGCCCCATGTCCACATGTCCC
TGTGTTCTCATGTTCCCATGTCCCATATCCCAGTGTTCCTAACCCCATAT
CCTTGACCTTGAGCCCATACCCTGATATCCCTGACCCTGTCCCCATTCTC
AGCCCCAGTTTCCTGCTGGGCCCCCACTCATGGTTGGAGGAGGTGCCATC
CCCTGGACGCTGTAAGGCCACAAGGTTGCGGGGTTACTGCGCCCAACTGC
AGGAGTTCCGCACCCGCTGAGCCAAGTGGGCTGCCAGCTGTGAGCCCT
GGGAGCCACTGGGAGCATGTTGGGTGCAGCTGGGACCATTCTGGGGGTGA
ACTGGTACCCTGTTGGATCAGTTGGGATCAATTGGGAATAAACTAGTGT
TGACTGGGACCGTGTGTGACCAACTGGAAGTGTGTTGGAAGAACTGAG
AGTGTGTTGGGTTGAGTGGGAGCAACTGGAAGTGTGTTGGAACAAACAGG
GGACCAACTGGGATCACACTGTGGTCAGCTGGGATCACACTGGGTCAAAA
AAGATCACAGTGGCCCAATTGGGGTCATACTGGGGTGAGCTGGGATCAGA
ACGAGTTTAATAAACGTACAGTCGTCCGAGCCACCACAGAGTCAGCCCTC
CAGCGGCGCAGAGCGGCGCAGCGCGCACTGGCTGCCCGCGGTAAGCGGAT
GTGACGTCACCTTCGCGGCGCGCTATTGCAACTCCAGCAGCGCCCCGCGGA
GCGCCCCAATGCCGCGGCCCAAACCGCGCAGCCCCCGCGCGCGGGCGCGC
CCCCCCCCGCGCGCCCCCCCCCGCCACCCCCCGCGCGGCTCGCGGTGAGTG
CAGCCCCGTAGGAGTGCGGAGTGTGGGGGCGGGGGGGGGGGCGTCTGGAGC
GGAGCCTTTATCACCCTGTGTTTCCCGATTTCCTCCCTTTTCGCCCGT
TTCAGCCCCGCGGTACCGGCCCCGCTCAGAGGGCGCTGCGGGAGATCCGCC
GCTATCAGAGCAGCACCGCTCTGCTGCTGCGCCGCCAGCCCTTCGCGCGC
GTGGTAACGGGACTGCCCCGGAACGGGACACCCCCCAACCCCCCAACGG
GACCATCCCCCACGGATGGATCCCCCCCCACACACATCCAACGTGGGAC
CCCCCGCCCCAAAATGAGATCTCAACGTGAGATCTGGGGGCTCAAAATG
AGACACTCTCCCCCTCCCCCAACGGAACACCCGAAAATGGGACCACAC
ATAAAAGTGGGGACTCCCCCTCCTCCCCCGCGCCCGTCAAAATGGAACAC
CCCCAAGTGGACCTTTCAAAAAATAACATTCCCCTCCCCCAAAAATGGG
ACTTACCACAAAGTGGGATCTTCCCCCAAAATGAACACCCCTCAAAATG
AGACCCCTCGGACCCCCCCCCAACCCTCTGCACCCATCNGCCGTCTGTGCA
CGGAAGGGAAAGGCTGTAGGGTACATCTACCCTTATTTCTTGGGTTTGTG
TTTGTGTTTGTGTTATTTAGAAGCAAAACCAAGACAACAAAGCCCAGCC
AATGCCATTTCTGGCAGTGGACGCAGGCGCAGGCGGGTTGGTCACAAAG
CAAGAAGTTGCTGCGGGACTTTGTGCTTTTGGGGCCGTTCTCGTGAACCT
CTGAGCCATGGATGAGGAAATTACTTATGCTGATTAAAGGCATCCTACGG
GCAGTTTGCTCCTGCTAAGCGGCAGCGCGGTAAGGGATGCTCTGTGTGG
TGGGTGCTCACCAGGCTTGGTTTGGGGGCTTGTGTTCTCTGAGAAAC
ACCAGCAATGCTGGTTGGGTTCTGGGTCCACCTGGCTTGTATGGGGGAG
TAAAGGAAGGGGTGGGGGAGAAGGAAGCCTGGGAATGGCCAGAGGTGTGG
TGGTTTT

FIGURE 10

SUITE 7

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Conti131.txt

AGAAGAGCCCCGTGATGTCCTCCAGGTGCGGTCCCTCGGTGCCTGTGGGG
ACAACGACAGCCCTAAGCACAGTGTACCATCCTGGGTGGGGTCCCCAAC
CCAAATCCATGATCTCCCATTTGTCCCAGGCCATGGTCCTGATGTCCCTCA
GACCCTCCTAACCATGGTCCCAGCATCCAATACTCCACGTGTTTCCAA
TATCCCCACATCCCCCTCACCAGCCAGGAGCAGTCGGACGGAGACACGC
ATTGGTTTGGCCAGTGCAGTGTGGGTGACAACGCAGCTGTAGATGTCCCC
GTGGTGTGGGGGCGTGCGGGGATCAGCCGTGCTGCCGCGGTCCGGCTGT
AGGTTCCATCGGCTGCCTGGCGGTGACCTGAAGTCCAGCTGTCCATCACT
GTGTCCCTGGGTGACTGTGATGTCCCCGAGCCCCCGGCGGGCGCTGCCA
CGTCACCGTCACATCCAAGGGGTAGAAGCCAGACACGTGGCAGCGTAGCT
CTGCTGACGTCCCCGGGGCCACCACCAGGTTCTTCGGGGACAGCGTCACC
TTGGGGGGCTCTGGGAGACATGTGGGGGGACATCGGTCCCATATAGCCCA
TAGGGCCCCCTCCTATAGGGCTCATCCCCCCTATAAACCTACAGGTGAAC
TATGGGATGATGCCACCCCATCCTATAGTCCTCATAGGAATACCACCCGG
TCCCATCCACCCTATAGCCTCCATAGGAATACCACCCAGTCCCATCCACC
CTACAGCCCCCAGAGGAATATCACCCAGTCCCATCCACCCTACAGCCCC
CATAGGAATACCGCTGCTCCCATATGTCCTATCTGACCAATAGGAATAC
CACCCAGTCATACACACTCCGTAGGAACACTGCCCAACCCACACCCCAT
AGGAACACCGCCTGCCCCACATGGACGCACCAAAGACGTGGAGCTGCAGC
ACTGTCTGTGTGTGCCCGTGGGGCAGGAACACGGAGCAGATGTAGGTGCC
CTCATCCCCCGGTGATGGCCGCGCCAGCCGCAGTGTACCGCTGTCACCC
CGTCCCCATCCCGTGTCCCCAGCAGCAGTTCGGCCCCGGGGGTGGCGCGG
GGGGCGCGGGCGGTGGAACCTGTCATAGG

FIGURE 10

SUITE 8

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AB1B3FOR.txt

CCAACTTCCTTTGGTTCAGGGAAGAAGACTCACCCACTGCTTTGGTTTGT
TGCACTGGAAAAGCATGAAGAAAGCACCACATGATGAGAGGAACAGTTCA
TCCCACAGCTCACGCAGGAAGAACCCATTTTAAATTTAATTGGGAGGGA
GCACTCACCCAGGTCTGAAGCTAGTTTATCTGCAATGAAACAAATAAGAA
ATGCATGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCCCATGGGA
AGACCCCGAATCTCTTTGGTTTGCGGAGGAGGACTCACCCAACGTGTCAT
TCCTTCCCTCTGCAAAGGGAAAGCAGAAACAGTG

FIGURE 10

SUITE 9

47/110

AB1C1FOR.txt

TGGGATCAAGTTGAGTAGACATAGCATCCTCGCTTTTAGACAAGACCTGC
ACAGTATACCACCGTTTACTGTGCAGATAATGACCAAAAGCAATATGCGT
CACACTTTTCTGGTGACAACGTCACAAAATGGCGGTCGTCAATCGTGACG
AACAGCACAAACGCCCTTCTCATCGAAGATTTCAATCTGCCAGACCTGG
TGACGCGAACCAGATGCAACGGTTTGCATACGCCGCGCACCCGCCCTTC
TCGTGCCGAGCGGACGTGGTTAGCATTGATTCCAGACCAACCACTTTT
GCTCACCTTCGGTACATAAATAACCGGCAACGGAACCGATACTTTCGGCC
ATTACCACGGGTGCTCCTCCATGCAGCAACCCGAAAGGCTGCTTTGTCCG
CGAGTCTACTGGCATTTGTCGCTTCAAGGGTGTCAACCAATATGTTCAA
AGCGAATATCCAGGAACCCACCATGTTTCCTTACCCATAGCATTCACT
GCTTCCAGGGTGATTTTCCGTTTCCAGATCATTTAATAATCTCCAGTTAA
AGCCTGCACAGGATGGCTTACCCCGTGCCTTCAACCGTTTTATCTGGCT
ACGGCAAGGAATATCCGTT

FIGURE 10

SUIITE 10

48/110

AB3A11RE.txt

CCGTCGCCTCGGCTCTCCCTCGGGCTCCACCCCCCGTTCCGCCCTTTG
 CCGCCGCATCTCCCGCTCTGTACCTCCCCAAGAAGTCGCTCAGACGGCG
 TCGCGTTGTCTGCACATCCTCGGGGACCGTCTGTTGTGCGGCAGCAGGGG
 AGGGGAGCGGGCGGTCTGTGCTCTTCTATTCCCTTCAGTACAAGAAGGTG
 GTTTGGGTTCTTTAACCAAATATACTCTTTTGTGTTTGCATAAAATCACC
 AGAAGGAATTGGTCTGTTGAATATATAGGAGTGGTGGAGAGAGTCGAAGA
 AGTGTTTCCTGTGACAAAACACCGTTAAAAGTGAATTCATGGAGAACGCA
 CTGCAGTGACACAGAAGGGAAAACACGAAACATAAATAATTGCCGATT
 ATCATCGATTTCAGGGTCCTTTGGGCTGATTGCTTTCCAGTATTTCCCT
 TTGGAGAAAACCGGTGAAAAATGG

FIGURE 10

SUITE 11

49/110

AB5B6FOR.txt

TCACCTGGCTTTGCTGCTCCAGACCCCGCAGGAAGCGACCCCCCTGGCCC
CTGGCATCCCGCAGCCCCACACGCAGCTGTGCACGGCCCCACACTGGCGC
CCCATCTGGGAATCTGGGGGTCCAAAGGGTCAGTGGAGTCAGGCGGGTCC
AAAGGTCAGTGCGGT CAGGAGGTCCCCAGATGTCAATAGGGTCAGGGGGA
GGGATCCCAAAGGCCAATAAGGTCAAGGGGAGAGATTCCAAAGGTCAGTA
GGGTCAAGGTGCCCCAGAGGTCAATAGGGTTGGGGGAACCCAAAGATTAT
AGGGTCAAGGAGTGACCCCAAAGGACATCAGGGCCACTGATTTGGGGTGG
ATGGGAGAGGAATTTGGGGAGTTCAGGAGAGTTGGAGGGGATTTGGGAGG
TTTTGGAGGAGACAGATGGGGATTTTGGTGGGAATTTGGGGAAGATTGGG
TGGGATTTGGGATTTGGGTGGGATTTAGGTGGGGATTTGGGGGGATTTTG
TCTCTGGGTGTCCCATAC

FIGURE 10

SUITE 12

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AB6E4FOR.txt

CCTGAAACTTTGGGGTGAGCATCTCCATCAGCTCATCTGCAATGCAATGG
GATCTTCCAGTCTTTGGGTTTTGTGCTCGTTGTGCCACTATTTTCATGGC
ATCCTAAGATGGTGCTGTATTATTTTTGTGACACTGTAAGAGACTGGAGC
AGAAATTTTGTACAAATTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

SUITE 13

51/110

AB6G8REV.txt

GTTCTATGATTTCTTTGGTCCGAATACCATGAAATCTGATATTTCCATTT
CAGTATCTGAACTGGGTTCTCTGCTGGATCACAGTGGTCCACACAAAGAA
GCAGAACAGTATATCGCTCGCGTCTTTAACGCAGACCGCAGCTACATGGT
GACCAACGGTACTTCCACTGCGAACAAAATTGTTGGTATGTACTCTGCTC
CAGCAGGCAGCACCATTCTGATTGACCGTAACTGCCACAAATCGCTGACC
CACCTGATGATGATGAGCGATGTTACGCCAATCTATTTCCGCCCGACCCG
TAACGCTTACGGTATTCTTGGTGGTATCCCACAGAGTGAATTCCAGCACG
CTACCATTGCTAAGCGCGTGAAAGAAACACCAAACGCAACCTGGCCGGTA
CATGCTGTAATTACCAACTCTACCTATGATGGTCTGCTGTACAACACCGA
CTTCATCAAGAAAACACTGGATGTGAAATCCATCCACTTTGACTCCGCGT
GGGTGCCTTACACCAACTTCTCACCATTACGAAGGTAAATGCGGTATG
AGCGGTGGCCGTGTAGAAGGGAAAGTGATTTACGAAACCCAGTCCACTCA
CAAACCTGCTGGCGGCGTTCTCTCAGGCTTCCATGATCCACGTTTAAGGTG
ACGTTAAACGAAAGAAACCTTTAACGAAAGCCTACATGATGCACAACAAC
AACTTCTCCG

FIGURE 10

SUITE 14

CCACCACCGCTTTGGGCAGTGCCAGTGCTCCTCACAGGCTGTGGGGCAGA
GCAGGTGACCCCCAAGGATTTCCCCTACAAAGAGCCCCACAGAGACAGA
AATCCTTCACCTGAGCTGCAGCAAGCGCGGGCTACACCCAGCATCAATC
TTTGCCCAGCTTCTACCTTTGCCAGCTTCTACCTTTGCCAGCTCCAGG
GTGCAATGCGAGCAACTTGGCATCAGACCAATACAGTCAAAGGTTGGAGA
ACATAAAACACATCCCATTGCAGCTTTGTGCACCACCTGGGTCTCTGCT
ATCACCAGGAACATGGACACAGGAGAAGCTTTGCCATAGCACAGGAGAAA
GCTGTGCGCTGCACCTCATGAGCATTCTCTCAATTTCTCCTGTATCCCA
CAGGTTACAGGCACCAAGTAATTCTGCCAGAGCTATTCTGAAGGGCACGTG
GTGAAGGATTATGGCTTGGAGCAGTGGGGAGAGCCAAAAGCCCTTCCAC
ACTTGATGCACTCCAAGGGTGTGATCCAGCATGCAGCCTCTCATGTTGG
AATGGTCAATTTTATCCTAAAATCCTCTTGCACTTGGAGCAATGTTGAGT
TATTTTCCCCATGTGCATTACAGTGAGGTCCCCCTGAAGCCTACTCTTC
TCCAGCCAATTTCTTATGATCACGAAGGGGATGATATGATGGTGACATGG
GGGATTTCCACGTGGATGCTGCAGGGCAGATGGGGAAGGGGTGAGGGGAG
ATGCCACAGCAGAGTTCCCAATCAGGACACAGCAGTTTGTGCCAGC
ACCAGGAAGCAGCTTCCCCCTCCTTTCCCTGCTGGGAAATCACTCCTTTGG
AATGTTTTTTTTTTCTGCTGCTCACCCACATTTTGCACAGGGCTGATCT
TCCAGGTGAGCCCAACTCTGCATCCCCGCACGGATAACCTCTCCCTCCC
TAAGAATCAGTGATCCTGCCTGCCTGCAAAGCAGCTGCTGAGATGTCTT
TTGCAGCCCTTATTCCCGCAGACCCCGTGCAAGAACACACATCTCCAT
CCTCTCCTCCGTTGGCAAGGAATGGGTTTGCAAAGGGATGGGCACAACCA
GCAATATGCAAAGGAAGAGGTGTGAAAGTCTGGGGAGCAATGAATCTGT
CCCCCGAAGATGTTTCCATGGGGCAGTTAAGGAGGAGAATTGGAAATGA
AGCAGATGATGCAGCAATGAAACTATCCAGAAAAGGGGGGAAAAGCAAT
TCTGGTAATGAAGATACATAAAGGAGAAGGGCTTCTCGCTGTCTGGACGC
AGTTCTGTTGGTTAACGTCTTTTCTTTTGCTCTTTGCACTTTTTTCT
TTGCTGCTCTGGTCAGGATGAGGCAGAGCCCTCACGGGGCCCTTTCACA
CCTTTTTTTAGCACACAGAAGCGCAGCGCCGTCTCAGCACCAGCATCG
ATGAGAAGGGACTGCAAATAAATTAATGCGTTACTGAATAGACAGTCGT
AATTAAGGATCAAAACCATCCCTCCAGTATCCAGCTGCCAGGCATC
GGTTGGCACAGAATCACCAATATTGCCTTTCTTCCCCCATCCCCGCTTA
TCAGCCAATGCTCTCTGACCCCTAAAAGGTCTCGATTTGGGGTCTTTTTG
TTGTTGTTGTTGTTGTTCTGGGTATTTTTAGGCTTTTATTATCAGCGATT
TTTCAGCTTCTCACTGTTACCCCCCAGCTCAGCACCAGCATCGCTCACTG
CCATCGCTGAACCCAGCGGCGTTTCCATCCCTCAGAGAGCAGCAAAATGA
GACATCGGCCGTGCTGCAGGAAGGGAAAGGCTGTAGGGTACATCTACCC
TTATTTCTTGGGTTTGTGTTTTGTTTTGTTGTTATTATAGAAGCAAAACCA
AGACAACAAAGCCCAGCCAATGCCATTTCTGGCAGTGGACGCAGGCGCA
GGCGGGTTGGTCACAAAGCAAGAAGTTGCTGCGGGACTTTGTCGTTTTGG
GGCCGTTCTCGTGAACCTTCTGAGCCATGGATGAGGAAATTACTTATGCTG
ATTTAAGGCATCCTACGGGCAGTTTGCTCCTGCTAAGCGGCAGCGGGT
AAGGGATGCTCTGTGTGGTGGGTGCTCACCAGCAGGCTTGGTTTGGGGCT
TGCTGTTCTCTGAGAAACACCAGCAATGCTGGTTGGGTTCTGGGTCCACC
CTGGCTTGATGGGGAGTAAAGGAAGGGGTGGGGGAGAAGGAAGCCTGG
GAATGGCCAGAGGTGTGGTGGTTTTGAGCAAAAATCAGCCAGATCGGGA
AGCCCAATGTGAGAGAATGGAATGAAATGGTGGCAACGCACCCTGCATC
CACGTGGCATGAGGGCTGCAGACATCCCCGCCCTCCAGCCACCGGCTGC
CCCACACTGGGCTCAGCTCACAAAGCCTGGGGGCTGCTCAGCTTCCACCC
CATGCTCTATGGAGCCTGCAGGGCCTCCACCACCTCCAGAACCACACGTG
GAGGTGATGTCCCTGTGTCCATCTGACCTCCAGCGGGAGCCCATCCCATG
CTCCCTGCTGCTGTACCCCTCTGTGCCACCTCCTTCCCAGCTGGGAACC
ACTGGGAGCCACTGGGAAGGGTCCAGGGGACCCTGGAACCTGGAGGAAAAC
AAACAGGCATCAACTCTGCTCATACACAGCATGGGAACCAATGGGAAGG
GTCCGGGGACCCCAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

FIGURE 10

SUITE 15

53/110

B5FOR.txt

ATTTGTTGTTTCAGCAGAATGCATCTGTGTGCCCCATCCCCACTCCACTTC
ATTTCCCTTTCTTTTCCTGCAATAGGAAATCCATCTTGAGGGGACGGGGA
CACAGGCAGGCTCACAGAGGGGACCCTGGGGTAGCAGTGCCGGATTGTTGGG
CTGAGGCCCATAGCAGTGACCACAGAATCGGTCAATTTGTCGGTTCATGGT
GAAGATGGGAGGGGTTTCAGCAGAAGCACTCCCTGGGACTCCCAGAGGGC
TGTCTCAGAACCCTGCTTTCTTGCACAGAAGATGAACCATTTTGTAG
GGGAGGGTCCAGGATGTGTTGCAGTGTGAACAAAGCCTGTGTGCTTTT
ATAATTCTCTTCTGCTGCTGCTGCTCATTCTGAGGGCTGAATGGGCAG
CACGGGCAGACAGCAGCGTGGCTCCGACACTTCTATGTCTGCAGTGCCCA
TTGCAGGAAGAGAAAAGAAATGGAGTGGGGATGGGGCAAACAGATGCATT
CTGCTGAACAACAAATCCGGTATTTTTTTATTGAGAGAAATAACACAGGA
TTGTGAGCTGATTGCATGAGCGCATGCAGCGATGTCCCCCGTGTGCCCG
GGCAGTCTGGGGTCTGCACAGCCCCAACTCCTCACAGAGCCGTATTGCA
GAGCTTCACCCCAACGCCTGGGGCTTTTGGGGTGGGCACACATCAGAGGG
AGGGACTGCGTTGCCCTCCATCTCCTGCACATTATGGATGGAGACGTAAA
GGTCTTTCTGGCAGACCCACTGGTGTTCACCACTACAGACGTGCCCCC
CACTTTTGTGTTCTTGAAGGTCCCGCAGCGATTCTCCATCACGGAAGGT
TATCAGACCTGCAAAATAAGGCTGTTTGCACCCAAACACCCGACTTGAAG
GAGGCGGGCAATGGTTGCAGAAATACTCACTCTGTGCTGTGTAGGAGGA
GTTGTCCACCCATTTCATTGATTGTGGACACTTCTAATCCAATCCACA
CCGGCTCCCGCACTGCCATCTGCTGGAGGTGATCCTGGGAAATGGCACC
AAATCCTTCTGCAAGGGGCTGGAGGGGTGCAGAGCCACCAAGTCTGCCTT
GTTGGACCCCCAGCAGATGGGACTCAGACAGCAGCCATGCCCTGGAATGCT
GCCTGGCTCTGCAGGCGGCTCAATGGGTGGGAATGGCTTCAAACCCGAGA
TGGAGGCACCGGTGTGACCAGCTGAGCTCTGCTTCCATCCTTCAGCCTGT
TTGAAGGGTGGGAGGGGACACAACCCCATGTCCCACCCCTAGCCTGAAC
CTTGATGTCCTTAACCTCAAACCATATGTGCGCAACCCAGCGTGCCTGA
CCCCAACCCGTGTGCCCTACTGCCATGTGTTGACCCCTAACCCCTAAAGGGC
ATAATCCAGACCCCAATCTCTCCAGTGATGCTTTAGCCCCATTGCGTTT
GGAACCACTGACCCTCCTGCTGCCGCCAGTCACTCCAGAGCGGTTTTCT
CCCACAGAATCCACCAACCCACACATTTTCAGGTCCCGTCCAGCTCCCT
GCTCTATGCTTACCTCTTCTGCCTTCTTCCGGAGCACAGCCAGCTGAGAC
TGCAGATTTTCACACTTCATTTTTGCTTGTGTCCAGTTCCTTTTCTGT
GGAAAGCTCATAGCATCGGTCCCCTAAAAGCCTCCAGAACTGGGGACAGA
GCAGGCAGGCAGGGGCTGGAGAGAAAGAGCCGTGAGCATCTTCAGGT
GGGAGAAATCCCACCCAGGAGGATTTCCTTGGGAAGGGCATTACCTGCAG
AGCTGTTCCATGTGGATTGGCAGAAGTACTGCTCAATGGAGGTATTCTCG
CAGAGCTCTGTCCCATTCCTCCCGTTGGTCTCAGGGCAGTGCCGGGCAGC
GCTTGGAGGTGGTGTGTTTTCTGAAAGACTTTTGGGCACAACCTGGGGT
GAGACGCGGCCCTATGGGGCCAACCCGTGGAACACGAGGGTGGGG
TTGGATCCTCGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCACTCA
GTTAATTAACTGTCTAAAACCATATTTGTATATAATTAGACATGATGT
TTACTGCTTCTGCTCCCCCTTGGTTTAAAGAGCAGAGAGGCTCTTGCAGA
AGGGAATTCTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATCACC
AACTCCAGTGCAAAGCCCCAGCCCCACTTTGGGCAGAATGAATGTGTTT
TCTGCTCAGAAGAGCTTCGATTTCTGTGCAGCAATGTGGTTGGGATCTG
ATCACTCACCGCACACGCTGAGCCCTGTCAACAGCAGCAGCAGCAGCAGC
AGCAGCACCCCCAGCATGCAGGCTTCTGGAAGTCCCACGGAAGTGAAG
AGCCCACTTATATAAAACAGACATTTTGAAAAAATTTTCTTTTACA
GAAATGATCTCCCTGTGAAAGAGCCCCCTCCACCAACCTGCTACGTTAGAG
CAGAAGTTGATGGCTGCTTTGGTTTCTTGAGAAATTGGGGTCCCCGACC
CTTCCCATTGGTCCCATGCTGTGTATGAGCAGAAGTTGATGCCCTGTTT
TTTTCTCCAGTTCGGGGTCCCCCTGGACCTTCCAGTGGCTCCAGTG
GTTCCCAGCTGGGAAGGAGGTGGCAGAGGGGTGACAGCAGCAGGGAGC
ATGGGATGGGCTCCCGTCCAGTCAATGCAAGGCAATCACTTC

FIGURE 10

SUITE 16

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B5FOR.txt

ACGCGTGGTTCTGGAGGTGGTGGAGGCCCTGCAGGCTCCATAGAGCATGG
GGTGGAAGCTGAGCAGCCCCCAGGCTTTGTGAGCCGAGCCCAGTGTGGGG
CAGCCGGTGGCTGGGAGGGCGGGGATGTCTGCAGCC

FIGURE 10

SUITE 17

55/110

B5REV.txt

CCCAGAACCCAAACCAGCATTGCTGGTGTCTCTCAGAGAACAGCAAGCCCC
CAAACCAAGCCTGCGGTGAGCACCACACACAGAGCATCCCTTACCGCG
CTGCCGCTTAGCAGGAGGCAAACCTGCCGCTAGGATGCCTTAAATCAGCAT
AAGTAATTTCTCATCCATGGCTCAGAAGTTCACGAGAACGGCCCCAAAA
CGACAAAGTCCCGCAGCAACTTCTTGCTTTGTGACCAACCCGCTGCGCC
TGCGTCCACTGCCAGGAAATGGCATTGGCTGGGCTTTGTTGTCTTGGTTT
TGCTTTTAAATAACAACAAAACAAAACAAACCCAAAGAAATAAGGGTAG
ATGTACCCTACAGCCTTTCCCTTCCGTGCGCAACGGCCGATGTCTCATT
TGCTGCTCTCTGAGGGATGGAACGCCGCTGGGTTCAGCGATGGCAGTGA
GCGACGCGGTGCTGAGCTGGGGGGTAAGCAGTGAGAAGCTGAAAAATCGC
TGATAATAAAAGCCTAAAAATACCCAGAACAACAACAACAACAAAAA
GACCCCAAATCGAGACCTTTTAGGGGTGAGAGAGCATTGGCTGATAAGCG
GGGATGGGGGAAGAAAGGCAATATTTGGTGATTCTGTGCCAACCGATGCC
TCGGCAGCTGGAATACTGGGAGGGGATGGGTTTACTTTAATTACGGCT
GTCTATTAGTAAGGCATTTAATTTATTTGCAGTCCCTTCTCTCCATGC
TGGGTGCTGAGACGGCCGCTGCGCTTCTGTGTGCTAAAAAAGGTGTGAA
AGGGCCCCGTGAGGGCTCTGCCTCATCCTGACCAGAGCAGGCAAAGAAAA
AAGTGCAAAGAGCACAAAGAGAAAAGACGTTAACCAACAGAACTGCGTCC
AGACAGCGAGAAGCCCTTCTCCTTTATGTATCTTCATTACCAGAATTGCT
TTTTCCCCCTTTTCTGGGATAGTTTCATTGCTGCATCATCTGCTTCATTT
CCAATTTCCCCTCCTTAACCTGCCCCATGGAAACATCTTCCGGGGGACAGAT
TCATTGCTCCCCAGACTTTTCGACACCTCTTCCTTTGCATATTGCTGGTTG
TGCCCATCCCTTTGCAAACCCATTCCCTTGCCAACGGAGGAGAGGATGGAG
ATGTGTGTGGTTCTGTACGGGGTCTGCAGGAATAAGGGCTGCAAAAGACA
TCTCAGCAGCTGCTTTGACAGGCAGGATGCACTGATTCTTAGGGAGG
GAGAGGTTATCTGTGCGGGGATGCAGAGTTTGGGCTGACCTGGAAGATCA
GCCCTGTGCAAAATGTGGGTGAGCAGCAGAAAAAAGAAAAAATTC
CAAAGAGTGATTTCCAGCAGGGAAAGGAGGGGAAGCTGCTTCTGGTG
CTGGCAGCAAACTGCTGTGTCTCCATGGGAACCTCTGCTGGTGGGCATC
TCCCCTCACCCCTTCTCATCTGCCCTGCAGCATCCACGTGGAATCCCC
CCTGAAAAAGCCCATTTTGTGACCATGCATCACATTTATTTTCGCATTCA
GCATCAGCAGCTGACAGGCAATGGGTTGGGGGATGGGGGGGGGCTGAG
GGTATATCTTTTTGCTGAGCCAGGTTTTGAGTCATGGGGGATAATTTTAT
TCCAAGGGGAGGGGGGCATTTAACTGCAGGTGGTAACAATGAAAGGCAGT
GGGAGTTGTTGTGATTGCATGGGGGAAAGCACTGGTTTTTTCCATAAATT
GGGACTGATGTGGCTGTTGTTGCTTATTTTTATGGGGGAGGTTGTGGGG
TTTTTTTCCCCTATATTACATTGCATTTAATTTTCAGTCCCTCTCTCATTGT
CTATCCCTGGCAATGCTAGGACTTCTCCTTGCTGTTTTCTGTTGGCGAT
CATTGCCACAGAGGGAGGAATTGCTTTTCAATTGGGTCACTGCAATGAGT
TTTAGCACCCAGAAATATATCCTTATGGGTCTCTGCTTTTGGGGCACTGC
TGATGGGTGGAAGTTTTGGTTTTGCAGGTGAAGTGGAAGCCCCAAATGGA
GGAAGTGAGGGAATATCCCATGTTTGGGACAGAAATGGAGCAGGAGGG
AAGGTAACAGCCGAGCCATGCCCTTAACACATCTGTTTATTGTTATTATT
ATTGTTATTATTTTATTGATTACTTCTTTAACTTGAGAACAAGGGGAGG
GATGTGGGTGGGAAGAAATGAGTCTCATTTCTTTTAGCACTTCCCTCAA
GGGGAATTTGTGTTGGTTGTTGAGCAGCAGGTGGACTTCTTGCTGTGA
GCAGCCACATTTTGAAGAGTTCTGTTGTTATTAGCATTATTTATGCGAT
TCTGTGATGTTTTTATTATAATTAATTGTAATGAATCCTCCCTGAGGCAC
TGGATGGGGGAAAAAACAACATTTTGGGGTCTACTGCTCACACCTGG
GGTGCATGTTGCCCATTTGAGGTCCCTTCTCCCATAGGTCCCAGCCGTG
GGGCATGCGTTACCTTCCAGCTCACGATGGCAGCGGTGTTACAGTGCTG
CTCATCACTGCTGTTGCCCTTGCAGGTGAGTGCTGAGGGTTCCAAAGAGC
AGAGAAAACCCCTTTGGG

FIGURE 10

SUITE 18

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A52FOR.txt

TTCTCCACAGAATCCACCAAACCCACACATTTTCAGGTCCCGTCCAGCT
CCCTGCTCTATGCTTACCTCTTCTGCCTTCTTCCGGAGCACAGCCAGCTG
AGACTGCAGATTTTCACACTTCATTTTTGCTTGTGTCCAGTTCCCTTTT
CTGTGGAAAGCTCATAGCATCGGTCCCCTAAAAGCCTCCAGAACTGGGGA
CAGAGCAGGCAGGCAGCAGGGGCTGGAGAGAAAGAGCCGTGAGCATCTTC
AGGTGGGAGAAATCCCACCCAGGAGGATTTCTTGGGAAGGGCATTACCT
GCAGAGCTGTTCCATGTGGATTGGCAGAAGTACTGCTCAATGGAGGTATT
CTCGCAGAGCTCTGTCCCATTCTCCCGTTGGTCTCAGGGCAGTGCCGGG
CAGCGCTTGGAGGTGGTGTGTTTTCTGAAAGACTTTTGGGCACAACCTG
GGGTGAGACGCGGCCCTATGGGGCCAACCCCGTGGAACCACGCAGGGTT
GGGGTTGGATCCTCGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCA
CTCAGTTAATTAAACTGTCTAAAACCATATTTTGTATATAATTAGACATG
ATGTTTACTGCTTCTGTCCCCCCTTGGTTTAAGAGCAGAGAGGCTCTTG
CAGAAGGGAATTCCTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATC
ACCCAAACTCCAGTGCAAAGCCCCAGCCCCACTTTGGGCAGAATGAATGT
GTTTTCTGCTCAGAAGAGCTTCGATTTCTGTGCA

FIGURE 10

SUITE 19

57/110

H82FOR.txt

CTGCGCTGGGGATCTTGTTCCTCCCTGGCAATGGGAACAGCTGTTGGGTG
CCTTTTTTGGGAAAGATCTCTTTATCGGTGCATGAAGAATGAAGCGACTA
ATGGGGAATGGAAGGAGTGGTGGCTGTTTGAGTAATTGACTGATAGGTTG
ATGGAGGGATACTTGAATTAAGAGCTTTTGGCTCTTATCTCATTGCCTCT
GTGCACCAGGTTTGGAGTGGGCCAGGCCCTGGCACGGTCAACTTGCTCAC
TGTTGGCAATAGGAACATTTTTTGGCCCTCAGAGAGATTTTGTGGAGGA
ATGGATGGATCATTATGTCCTGGTTTGTCTGGGGGGGACCAATGTGATG
GATTAATTTTTTTCAGTATAAAAATAGTTTGTGAGGTGAAGTTCTGGTGA
CTGAGTGGATGGTTGGATGGAGGGATGTGAGTTTCTGTGGAGGGATGGAT
GGTTGGAAGGTTTGTGGATGCACTGTTGAGTGTCTGGTGGGATCTACATT
TGGGGCAATGGATGGATGGACTCTGAGAATATAGACTATAGCTGAGTTGG
CAATGACCAAGAAGGACCATTGCGTTTTGTTTCTGGCTTCATGTAGGATC
ACCCAGGAATTAACCCCTATGTCATGGTTTTGTAACCTCGCTATTGGTAT
TCCACATCATAACATCATGGACAAAAGAGAAGAATAGCAAAGTTACAAAA
CCATTGACACCCCTACTTCTGAAAGCAGTTTTGAAATGCTTGGGGAGCTGAA
TGGTTGATGGTGGTGGATGGAGGGATGTGAGTTTCTGTGGAGGGATGGAT
TCCCTGGGAAGCTATAGCTATAAGTCACCCCAATGCCCTCTGTGTGGG
AGTAGTGTGGGTGGGGTCACTGGGATACCACAGTGGGGTGGAGCCCAGG
GGAGTGTCTTTGAGGTGAGTGGGGGTGAGCAGGGCTCTCTAGAGGCCTT
TGGGGGGTCCAAAAGGAGTTGATGAGAGAGAGAGTGTGGGAGATCCATGG
GGGGGCTGCAGGCCTCAGTGCCCTCCATCTCTTGCCAGGTGCCCCAGGAA
CACTATGGGTGGGGACACTGTGGCCCCGAGTGCTCACCTGCATTGGGCA
CCTCCCATGTTCCCCCTGAAGGCTACAACCTCATCTATGGACCCCCCGG
TGGCCCCGTGAAGGTAATACCCCATAGCACTCCCTGAACCTCCAGGGGA
TCTCCCTGGGTATCTCCTGGGGTACCCCAACCCTCCTTGGGGACCCTGCT
CCCACCTGGGGAATCCAAAAGTCTCCACCACCCAAGCACCTAAGAAC
CCACTGCACCCCACTATCCCTTGAGGTCCCAATACTCCTTTTACAGCA
TTCCCATCCTCCTCCTTGGCCCCCTTTATGCTCTCCAGAGACATTAAACAC
CCCTGTAATGCCCTTAGGGACCCCTGCAGCAGCCCAATAATCCTCCCAT
GTCTACCTCGAGACACTGCAGCTGCCCTGAAGCAACATCCAAGGAGCT
GTGGGGCCTGGAGCCCACTGGACGCTATAGGTGCTGAGCTCTGGGGCCGGG
GGCTGGAGCCCTTGAGACCACCTTTGACACCCGTGAGCTGGGAAAGGGG
GTCCTGTGGGTGGGAAGGGGCACTTGGGTGGAGGACTCTGGGATACCCA
AATACCTGGATGATTTGGGGTGTCTGGGGACATATGGATGCTGGGTCTGA
AGTATGGAGGGGGGTACCAAGGAATCTGCATCCTTGGGTGGGGAGCTCTG
GGGGTTCCCAAGTACCTGAATAATGGGTACCTAGTTAGGGGAATGCCTTG
GGGTGGGGGGGGGGGACACAGCGGGATGCCCTCGTCCCTTGGTAGGTG
AACAGGGACACCCCACTGGTTGGGGCCACCTACACTGCTCTGTCCTTCAG
CACCCCTCCCCACCCACATCCCCGGGACTGCGCTGAGGAGCAGCTCAAT
GGACCGGGGCCTTCACGAGAGGTCTCATCTTCTCGGGGGCGACCGGCA
GCGGCCACTGCACGTCTTCTGCGACATGGAGAGCAATGGGGCGGCTGGC
TGGTGGGGAAACGGGGCGGTGGGGAGGGTGTCTGGTGGGCTCTAGGGGGT
GCTATGAGGAGTCTGGTGGGCAATGGGGGTACAGGGTGGGGTGGCTGAC
TCCATGGTTGCCATTATAAGGGTTGGATTGGCAATAAGAGACCTGTGGAG
CACTGGGGGCATTGGGGTATCTGGGGAGGTTCTGTGGGGGTGAGAAG
CAATGGGGGGGGGAGTGGGGGAGGCTGGAAGATTTAGGGGAGGTTAATG
GGAAGGTCTTGTGGGGCAATTGGGGTAATTCTGGGAAGTGCAGGGGGATC
CCAGTGTTCCTGTGAGATTCACATACCCCTATACTATCCATGGGGATCA
CAGTAACCTCTGGAAGTATAAATGGGGGAGAACCAGGGAGCAATGGGG
GGCTGTGGTGGATCTGGAGGGGCAATAGGGTGGCCCTGGGGGGCAATATG
AGGGTCTTAGGGTGCAATGTTGGGGGTCTAGGGGGAAGTAATGGGGGGTC
TGGGGGCAGTGGTGGGGTCTAGAGGGG

FIGURE 10

SUIITE 20

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Conti224.txt

GGAGGGAGCACTCACCCAGGTCTGAAGCTAGTTTATCTGCAATGAAACAA
ATAAGAAATGCATGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCC
CATGGGAAGACCCCGAATCTCTTTGGTTTGCGGAGGAGGACTCACCCAAC
TGTGCATTCTCTCTGCAAAGGGAAAGCAGAAACAGTGTGTGGTGAG
AGGAGCAGCTCATCCACACATCGCACAGGAAAACCCCTTTTTTATTTA
ATTTGGAGGGAGGACTCACCCAGTTCTGAAGCTAGTTTCTTTGCTAAAGA
AACAGATAAGAAATGCATGATGAGAAGGATCAAATTATCATCCCATAGGA
ATACCCAGATCTCTTTGGTTAGCGGAGGAAGACTCACCGAAGTCTGTGT
TTCTTCTCTCTACAAAAGAAAGGCAGAAACAATGCATGAAGACAGGAGCA
TCTCGTCCACAGCTCCCAAAGGAAAACCCCTTTTTTGTTTAATTTAAA
GGCAGCACTCACCCAGATTTTCAACTAGTGTCTCTGCAAAAAGAAATCAAAT
AAGAAATGCGTGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCCCA
TGGGAAGACCTTGAATCTCTTTGGTTTGCGGAGGAGTACCCCAACTTTGC
ATCCCTTCTCTCTGCAAAGGAAAAGCAGAAGCAGTGCGTGATGAACTGAA
CAGCTCATCCACAGCTCACACAGGCATCCCTCATTTTGTATTTTGTGTTG
GGAGGGAGGACTTACCCAGTTCTGCAGCTAGTGTCCCTGATAAAGAATCA
AATAAGAAACGCATGACGAGAAGGCTCAGGTTATCATCCCATGGCTGATC
CCATGGGAAGTCCCCAAATCTCTTTGGTTTGAGGAGGGAGACTCACCCAA
CTTTGCATCCATTCCCTCTGCAAAGGAAAAGCAGAAACAATGCATTATGA
GATGAATGACTAATTGCACAGCTCCCAAACATTAAAAAATAATAG
TGGGAAGGGAACTCATCCACTATCGCAGGTAGTTCTGCTGGAAAAGAAA
GAGCAGAGCAGTGATGGTCAGAGAGGACAGCTGCTCATCCACAGCTGA
TGCCATGGGGAGACCCTGAATTCCTCACTTTGGGGAAGGAGACTTACCC
AACTCTGCATCTTTTCCCTCTGCAAAATAGAAGCAAAGGAAATGCATGGT
CAGAGGGAACACCTTCTCATCCCATGGTTGCTCCCATGCCAATACCCCA
AATCTTTGTTCTGGTAAG

FIGURE 10
SUITE 21

59/110
Conti508.txt

CAGTGACAGTGCAGGTGGAGGGACACGGCGAAGGGACGCTGACGGTGGGT
GGCTGCATGGACATTGGTGT CATCTCCAAGACCGATGTCCCCTCACAACC
TCCCCTCATGGTGTCCCCTCATGCTGCCACGGTGTCCCCTGCTGTCCCAT
CATGGTGT CACGCTGTCCCCAGGTGCTCCGCCAGTTCCGCCTGCTGT CAC
CTCCGAACGCCACGTGCCAGGCGCTGCACCTGGAGGTGGCCATCACCGGC
CCCATCCTGTACCATGGT GAGGCCCCACCCAAAGGCCCGCCCCCTTTTC
CTCGCGGGGGCGGTGCCCTCAACCCCTGTTTTCATAT CCAACCCCAGC
AGATGAGGACTACGAGGACTACGAGGACTACGAGGAGGCGGAGCCTAAGG
AGGGGGAGGAGCCTACGGAAGGGGCAGTGCCCCGTGGAAGGGGCGGGGCCA
GCAGATGACCCCGCCCCCTCAGCCCCGTGTCCTTATGGGATGCCCGTAA
GCGGCAACGCCGCAGCACACATAACCCCTGCCACGAGGTGGCCTTCCTGG
TCTGCTTCCGGTGAGGGGCGGAACTTCCTGTCCCTGGGGGCGGGTCTTCC
TGCTGATGGGCGTGGCCTGTTGTAGGCGGAGCCAGGGGTGGCACTGACT
GGGATGGCGGTGGTGGAGATCACTCTGCTCAGTGGCTTCTACCCCATAG
AGCTGACCTGGACAAGGTAGGGGGCCAGGGGGACTTGTGGGACATGTTGG
GGGGTTGAGGGGAGTTATGGGGTGTGGGGTTTGGGGGTGTTGGAGTTGTT
GAGGTGGCAGAATGTTTGGGTGGAGTCATGGGATATGGGG

FIGURE 10

SUIITE 22

CCACTCTTGGGTGAGCTGACAGCGTCCCACGTCAGCCCCGACTCCGTCCA
GCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGGTGCAGT
ACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACGGTGGGTG
CGCACAGTGACCGTGCCCGGGCTGTCGCCGTCCCGCCGCTACAAGTTCAA
CCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCACTGATG
CTGTACAGGTGAGCATGCTGTGTTCTGCCTCCATGTTCTTTGCTTTCA
GTGTAGTTGTATGTGGCAGGAACCTTTCAGGGCCACTTTTGGTTAATGT
TGCCTTAATAGTCAAGGAAACAATTTGTTCTTGTGAGTGGGAATGCCTA
ACGGGATGGGAGTTTGGATGATGAGAGGACAAATCTTATAAGGGATGATT
GATAATTATTGCGGAACGGATGGAAGGAAGGTTGGATGGATGGAATGGTG
TTTGGATAAATTTGTGCTCAGAGCACAGCTGGAGTGTGGATGAATGTTG
CTTTGCTTGTGTAATGATGGATGTTTGGTTGTGTGGTTGCTTCCACTGA
GAATTCCTCCCTCTGTGCTGCAGCAGCAGCTCCAGCACAAAGAGGAGCCAC
CTTCCCCACCACGTCTGGGTGAGCTGACAGCGTCCCATGTGGCCCCGAC
TCCGTCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCAC
GGTGAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACG
GTGGGTTGCGCACAGTGACCGTGCCCGGGCTGTCGCCGTCCCGCCGCTAC
AAGTTCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTC
CACTGATGCTGTCACAGGTGAGGGCAGGAATTGGCACCTGGTGGGCTCTG
GGTTTGAGCAGGAGTAGAAATGTAAACGTGGCCTGCGCTGGGGATCTTGTT
TTCCCTGGCAATGGGAACAGCTGTTGGGTGCCTTTTTTGGGAAGGATCC
CTTAATCGCAGCATGAAGTATGAATGGACCAATTGGGTGTGGGTGGAGTG
ATGGCTGTTGAGATGAGTTGGTGGCTGCTTGAGTAATTGTCTGTTGGAAT
GGATGGACAGATATGTGAAGGAGTGAAAGGATGGATAAAGTAATTTAGGA
ATCGGTGGATGAAGAATGGGTAGGTAGACCCTTGGTGAAGTGGTAGAATG
GAAGGATTTATGAACAGATATGAGTTAATTCTTGCAATCGAAGTAGGTGTA
AGTGTCTATTAGCCTGTTGCACTGAACATGCAGTTGCATAGACAAATGAG
TGGGGAGAAGTACGGAGTAAATCCCTGCATGAATGGTAGGACAGAAACCT
GAATGCCTGGATGCTGGCAGTGTGAAGAATGGCACTTGGGATAGATGGTT
CGAGTATGGGGTAGATTAAAAGATGGATGGAAAAGAGGAACAGAGAGAGG
GTGATTGGATGAATGGATGGATGGTTGGATGTGACTGATTGACAGGTACC
AAGCTTTTTTCCTGCACTGTGCCTTCTGTGCTGCAGCTGCAGAAGAGACG
GAGGAGGAACCACCGTCCAGCCACGCCTAGGAGAGCTGACGGCATCCCA
TGTCAGCCCCAACTCCGTCCAGCTGGAATGGAGCATCCCTGAGGGCTCCT
TTGACTCCTTCACGGTGCAGTACATAGACGTGCAAGGCCAGCCGCAGGAG
CTGCACTTGATAGTGGGTGCGGCACAGTGACCGTGTCTGGTTTGTGCC
ATCC

FIGURE 10

SUITE 23

Conti534.txt^{61/110}

GCACAGAAGGAACCGCCATCCCAACCACGCCTGGGTGAGCTGACGGCCTC
CCACGTCAGCCCCGACTCCGTCCAGCTGGAATGGAGCGTCCCCGAGGGCT
CCTTTGACTCCTTCACGGTGCAGTACAAGGATGCACAAGGCCAGCCACAG
GTGGTGCCCGTGGACGGTGGGTGCGCACAGTGACCGTGCCCGGGCTGTC
GCCGTCCCGCCGCTACAAGTTCAACCTGTATGGGGTGTGGGGGCGGAAGC
GTCTGGGCCCCATGTCCACTGATGCTGTACAGGTGAGCATGCTGTGTTT
TGCCCTCCATGTTCTTTTGCTTTTCACTGTAGTTGTCATGTGGCAGGAACCT
TTCAGGGCCACTTTTGGTTAATGTTGCCTTAATAGTCAAGGAAACAATTT
GTTCTTGTTGAGTGGGAATGCCTAACGGGATGGGAGTTTGGATGATGAGA
GGACAAATCTTATAAGGGATGATTGATAATTATTGCGGAACGGATGGAAG
GAAGGTTGGATGGATGGAATGGTGTGTTGGATAAATTTGTGCTCAGAGCAC
AGCTGGAGTGTTGGATGAATGTTGCTTTGCTTGTGTAATAGATGGATGTT
TGGTTGTATGGTTGCTTCCACTGAGAATTCCTCCCTCTGTGCTGCAGCAG
CAGCTCCAGCACAAAGAGGAGCCACCTTCCCCACCACGTCTGGGTGAGCTG
ACAGCGTCCCATGTGCGCCCCGACTCCGTCCAGCTGGAATGGAGCGTCCC
CGAGGGCTCCTTTGACTCCTTCACGGTGCAGTACAAGGATGCACAAGGCC
AGCCACAGGTGGTGCCCGTGGACGGTGGGTGCGCACAGTGACCGTGCCC
GGGCTGTGCGCGTCCCGCCGCTACAAGTTCAACCTGTATGGGGTGTGGGG
GCGGAAGCGTCTGGGCCCCATGTCCACTGATGCTGTACAGGTGAGGGCA
GGAATTGGCACCTGTTGGGCTCTGGGTTTGCAGCAGGTAGAAATGTAAAC
GTGGCCTGCGTGGGGATCTTGTGTTTCCCCTGGCAATGGGAACAGCTGTT
GGGTGCCTTTTTTGGGAAGGATCCCTTAATCGCAGCATGAAGTATGAATG
GACCAATTGGGTGTGGGTGGAGTGATGGCTGTTGAGATGAGTTGGT

FIGURE 10

SUIITE 24

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Conti547.txt

CTGTGTCCCCAACCTGCTTGGTGTTCCTGCGCAGGACACGCTGGTGGCCCTG
GAGGCGCTGGCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGG
GCTGAACCTGGGGCTCTCCTGGCCGGGGGGTGCCCGGGGAGGGCTGGTG
GCACTCAGGTTATGCTGAAGCCGGGGCTGGAGCCGCTGGAGCAGGAGCTG
CAGGTGGGGACATGGCGGGATGTGGGGACACGAGGGATGTGAGGACACTG
GGGACATGTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATG
GTAGGACATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGAC
ATGATGGACACAGGGCTTTGGGGTCTTGGGTCTCGCTCTGTCCCCATG
TCCCCAGGTGCCTCTGGGCAGCCAGTGACAGTGACAGTGAGGGGACACG
GCGAAGGGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCC
AAGACCGATGTCCCTCACAACCTCCCTCATGGTGTCCCTCATGCTGC
CACGGTGTCCCTGCTGTCCCATCATGGTGTACGCTGTCCCGAGGTGCT
CCGCCAGTTCGCGCTGCTGTACCTCCGAACGCCACGTGCCAGGCGCTGC
ACCTGGAGGTGGCCATCACC GGCCCCATCCTGTACCATGGTGAGGCCCCG
CCCCCTTTTCTCGCGGGGGCGTGCCCTCAACCCTGTTTTGCATATCCC
AACCCCCAGCAGATGAGGACTACGAGGACTACGAGGACTACGAGGAGGCG
GAGCCTAAGGAGGGGGAGGAGCCTACGGAAGGGGCAGTGCCCGTGGAAGG
GGCGGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCTTATGGG
ATGCCCCGTAAAGCGGCAACGCCGAGCACACATAACCCTGCCACGAGGTG
GCTTCCTGCTGCTTCCGGTGAGGGGCGGAACTTCCTGTCCCTGGGGG
CGGTCTTCTGCTGATGGGCGTGGCTTATTGCTGAGGGGCG

FIGURE 10

SUIE 25

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Conti548.txt

CCTCTGCTGCTTCCAGAGCAAAGGAAAAGGGAGAGGGGGGCTCCCACCAC
CCTATCCCAGAGCATCAGATGGGCAATGGATGCAGCAGCTCCGTGGGTCTG
TGGAGGTGGCACGTGGCAGGAGCGAGGACGGCTCGGAGATACCGAGGTCA
TCAGCCACCGAAACCATCTCAGGAAAGGGAATTTCCACACAAAACCTCCAT
TTGGAGCACCTGGCAGAGAAGCTGAAGCTTTTGGAGCTGGATGGAGACAG
AGGGGAGAAGGAGAAACTCTGCTCGTGGCGCAAGAGGACATTCCCCTCCA
ATGGACCACGGGATGATGGAGGTCCCCTGGAGCCCCCATAAAGGAGTCA
GTGCAGGAGGATGTGGTCAGCCCTGTGTTATTCCCTAAAGCCCTGTTTAA
TCCTTCATGTCCATGCTGAAAACCTTCTTCTCTGCGAAGTCCAACACATTG
CATCTCTTCCCTTCTTTCTCCCATCACAATATCCTCCCCAAACCCCTTTT
TCTTCCTCCAGGAGCAGATTACAGCGATCTGGAGAACCTCAAGAAACAA
AAGGAGGAGCTCTTAGAACTCAAAGGAGTGGGGAGAGGCGATGCCAAGA
CCTTCTGGTAAGAAGCTGTTGCCTTCAAGCTGGAAAAACAGAGGTCTTTT
TGGGGTCCACGTTGTTGATTTTCCACAACCTACAGACACGGACGGAGGCT
GAGAGGCAGAAAATTGTGTCAGAATTCCGTCAGCTCCGCCGTTTTCTGAA
GGAGAAGGAGATGGTGCTCGTGGCACGGCTGGGGGAGCTGGACAGGGCTG
TGCTGAGGAGGCAGGAGGAGGAGGAG

FIGURE 10

SUITE 26

64/110
Contig51.txt

AGCCCAGCACTCTGCAGTCTTCTATCAGTTCCAATAGAGGAATTTTGGTG
GTAGAAGGGGCTGGAAGGACTCACTCTGCTTTGTGGTCTCAGCTGCTGGA
AAACAAAGCAGAGAAATAGCTGGTCAGCAGGGCAGCTTGGTTTCTGGGGA
CGTCTCCAGAGGGTCTGGACCTTTCCACCTGCCCCACGGTCCACCCACAT
TCCTATCTTTCCGCCCACACCCCTTTTCCCTTTCCTTCATTCCCAATCA
AACGGCAAATGTTATTTAATGACCACTGTCAATCCCCAGAAAAATCTCCC
TTTCTCCTGCATACCTCCACGGACCTGAGCTCAGCACCACCCGACCATC
CCTATCCCTGCTCAACACCTCCCTGTGATCCATCCCCTCCATGCTCAACT
CACCTTTCTTCTATAGAGAAAAACAGTGATGACAAATGACCCAACCAGA
ATTGTGACGATCACAGCCAGAGCCACCTTCCAGGGATGGGTGATCTGGGA
AAAGGGGTCTGGAAAAACATCAGGACAAGGGTTCCTTTTCCATTCCCAT
AAGTGGAAGCAAGACTCAGCCTTGGGACATCACAGAACCCAAAGGGGC
AGCAACCAGGGAGCAGTGATGCACAATGACGGCATCCCCATATTGGCACA
GGTGGAGGAGCTGCTCAGCATCGTGTGCCCACTGCCACTGAGCCATGGAG
AAACCCATCCCAGAAATCCAACCCAACCACCTCATCCATGCAGACTTATC
CACAAATTGCACTGTGCACCTGCTCCAACACCAGCATCTCATGGAACAAT
TTAGCTCCGACCTCTTCCAAAGGCTGCTGTCCTTCAGCTTTCATCCATG
GATGTGAGGATGAGGATGGACAGAGGTCGGGGTGGGACACACAAACCCAG
CAACACCTGGAGGCGTCACCCAGCCACTGACCTGACACCTCCAGGTCCA
CCACAGCGTCTGCA

FIGURE 10

SUIITE 27

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Contig99.txt

CCCAGCAAGGCCAAGCGCCGCCATAACGTCAGTGCCGGTGAGACTGTCTG
ATGCGGTTGCGCGAGGAGAGTCACTGAACATCGGTGATTAGGCGCAAAG
TATTTAGCGATTGATTCGAGGTTCAATTATGCGGCTTCCTTCTGTGGCTGG
TGGGTTTTGGTCTGGCTGTGCTTTACTATTGGCGGCATGCTGGCGCGCTT
AACGCTTTTCGGCCTGGTATCGGGTTATCTCGTCTCTGGTCATGATGGCCT
CCGATTCCAGGCGCGAATTGCATCGCGCTTTGTTGGATAGGTGTCAGTTA
TCGGCTTAATCAAGCATTGCTTTGTTGAACAACCGGCGTAGACACCATCA
CCATCAGAAAAAAGTTCTGCGCCGCCGCCACAGAACGGACACTCAAGCAG
AAAAGCCCAATGAGGTAGCTTGAGATCGAATATCATTGGTTTCATGCTGC
CTCCCGCTGTTTTAGTGCTTTGAGCTTGTCGCGGTACTCATCCCGGATCC
GGATGAAGTCTTCACGGCGGTAGTTGGTCATTTTCGTGGGGACCATTGAGC
CAGTTGACGTATCCCTGACCGTAACGAGCGACCAACCCAGCTTCGTATTG
CTGCGCCACGGTCGCCTCTTTGGCGGTGTAAGTGGCAGCTCCGGCATTAC
AGGATTTGCACTGCTTATGGGCGTTGCGTTCTTCAAAGCGCAGTTCAGGG
TAAGCACCTACTGTCTTGAAATGGCCGCAATCCCACTGGCCACCATGCAG
ATCAGGCGGATTGGTCTCGCCGCAGCTGATGCATGGCAAATCGGCGTCGC
GCGCACGGATAAAGGCGTTGAAAGCTTTCTGAGCCTGAGCCTTGTAGTAT
CCGTCTGGCCTGAGCTCTGCCAGCCGCTCCTTGCGGCGTTTGCGCCCGTC
CTTTTTCAGCCTCTTTTTGCTCCTTGATGCGCTTAGCCGCGGCTTTCACCT
TCTCCTTCTTGCGTTCTTCCATTGCGAGGATTGCGCCATGCTCCGGGG

FIGURE 10

SUITE 28

66/110

ContigB5.txt

CCCTATGGGGCCAACCCCGTGGAACCACGCAGGGTTGGGGTTGGATCCT
CGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCACTCAGTTAATTAA
ACTGTCTAAAACCATATTTGTATATAATTAGACATGATGTTTACTGCTT
CTGTCCCCCCTTGGTTTAAGAGCAGAGAGGCTCTTGCAGAAGGAATTC
CTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATCACCCAAACTCCAG
TGCAAAGCCCCAGCCCCACTTTGGGCAGAAATGAATGTGTTTTCTGCTCAG
AAGAGCTTCGATTTCTGTGCAGCAATGTGGTTGGGATCTGATCACTCAC
CGCACACGCTGAGCCCTGTCACCAGCAGCAGCAGCAGCAGCAGCAGCACC
CCCAGCATGCAGGCTTTCTGGAAGTCCCACGGAAGTGAAGAGCCCACAC
TTATATAAAACAGACATTTTGAAGAACTTTTCTTTTACAGAAATGATC
TCCCTGTGAAAGAGCCCCCTCCACCAACCTGCTACGTTAGAGCAGAAGTTG
ATGGCTGCTTTGGTTCTTGAGAATTTGGGGTCCCCGGACCCTTCCCATT
GGTTCCCATGCTGTGTATGAGCAGAAGTTGATGCCTGTTTGTTCCTCC
AGTTCCGGGGTCCCCCTGGACCCTTCCCAGTGGCTCCCAGTGGTTCCCAGC
TGGGAAGGAGGTGGCACAGAGGGGTGACAGCAGCAGGGAGCATGGGATGG
GCTCCCGCTGGAGGTCAGATGGACACAGGGACATCACCTCCACGCGTGGT
TCTGGAGGTGGTGGAGGCCCTGCAGGCTCCATAGAGCATGGGGTGAAGC
TGAGCAGCCCCCAGGCTTTGTGAGCCGAGCCCAGTGTGGGGCAGCCGGTG
GCTGGGAGGGCGGGGATGTCTGCAGCCCTCATGCCACGTGGATGCAGGGT
GCGTTTGCCACCATTTTATTCCATTCTCTCACATTGGGCTTCCCGATCTG
GGCTGATTTTGTCTCAAACACACACCTCTGGCCATTCCCAGGCTTCC
TTCTCCCCCACCCTTCTTTACTCCCCATACAAGCCAGGGTGGACCCA
GAACCCAACCAGCATTGCTGGTGTCTCA

FIGURE 10

SUIITE 29

CCGGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCCGAC
ATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGCTTG
TTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGGGGACTGTTGGGCG
CCATCTCCTTGCAATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTC
AACCTACTACTGGGCTGCTTCCTAATGCAGGAGTCGCATAAGGGGCATCGG
TCGACGGGATCACGTTGTGTCCCTGAAGCTCTCCTGTACCCAAACACAAA
GGTGATGTCCCAGCATCCCTATCCCAGCACTCTGGGGGACTCCTATTGA
ATTCTCTCCTTGGGCTTGCTGCCTTCTCTTCCCCTTCCCAGAGATCCCAA
AGGTTAAGCACCTTTGGGTGAGTGTTCAGAATTGTCACTGCCAGTTTGG
GGTATCAGTGGCAAATTGAGACCCCTTTTACCCAATCTTGCACTCTG
TTCCCCAGTCTTATGGTTTTAGATGGAGTAAAAAGGTTTATATGTCATAA
AGTTCTTCTGTGTCTGTTATTCTGCTGCTTCTGGATGCCAGGATCATGGG
GATAAGGGGAAAAAATGGGTTCTCTTATGCGTAGAGATGCAATCAGATG
GGGAGAAAAAGAAATCTTAATCTTCTGATCCATCTGACAGATATTCAGT
ACAGCCCTGAGGATGTGGGAAATAAATCTGAAGAGTTTGTGGCAGTTCC
AAGGATTTTGAATGACTAAATCCCATTCCTGGTGTCTGCACAAAGTTGGC
TGTGTTGGAACCCAGAAAGATCCATGCAAGTGGGTGATCCCTGAAAGCAT
TGTGTTCTGCTGTCTGCTAGCGGAGAGAAAGACACAGAGGGGAAAAATTAA
GTGTTTTATTGTTAATTATTGTACACTCTGAGGTTTCAAATACCAAATCT
TTAACGAGAGCGGACCACTTGATTTGAGGGTGACCATCTCAGATGGGGAC
AACTGTACCTGATCAGGCAAACCTGGGGGAAATTTGCCTTTCTGCCACTC
TTTTGGGTGGGATTTTCCCTTTTGACCACCATTTTCTACATTCTAATCAC
CCATTCAGCACTTCTCCCCCTTTTTTTTGCCCCATTTTTCTCCTGCTCA
GCACTTCTTAACAATATAATATAAATCAATATCATATCAATATGATTCTA
TGCCAATAGATTAATGGGGATGAAAGACACATAAAAACCCCAAGTCCTCAT
TTCATCTGCTTCCCATGGGATGGGTGGGGAGGTGGCTGTCCCCTGAGGCT
GTAGGATGTGGGGTCACCCCTTGTCTGTCTCAGGGACACAGCCTCAGCT
TGGACCTGACCCCTACCACCCACAGCCACGGACGGACCCCTCTCCCCAGAG
AAGGATGCATGGGAAAAAACAAGATGAGCCCCCTTCATCAGCATCAAA
AAATGCCACCGTCCCTCCAGCGTAGTCCAAGTGGACGCTGACCTCCTGG
GCACCCAGCGCAGAGCTAACAGGGTCACTTGTGGGTGGTGAAGTCCCCG
ACCTGTCCCCCCTTTCTCCACCCCCCAAATCCCCCTTTGGGACAGAG
GCTGAGTTGACCTTCCGAGGGATGGATTCTCGGGCCACACCGATGGCCC
AGTCCCCCTCATCCCCACTTCCACCTCCAGCAGTGCCGGCCGGCAGAG
AAGCTTTGGTGGCCCAAAACAAGGGCCAGTAGGCGAATCTTTCGGGTT
ATCAGGAAGGTCTGTTGTCCTTCCCACGTTTCACTCTTTCGGTCTT
CGGAGAGGATGAGGTCAGGGTGAGCGGTGTGGGGTCCAGGGTGATGCTG
GCTGTGGGGTGGAGAGGATGAGGAGTGTAAAGTTTGGGTCTCGGTGCTG
AGGCCATGAGGATGCGGAGAGCTTGGATCTCCAGCACTAAAGGAGTTGGA
TGTGCTCTAGATGGCCCCACCTGAGTAGGGTTGTAGGGTGGGACCGTCCC
TTCCAACCTCAGCCATTCTGTGGGGCCATGGGTTGGCATCGGAAGGGTAA
AAAGTACCAAAGAAGAAAGTAAAAAGGTGAGAGGTGGAACCCCTCTCAT
GTGCCCGTGCTATATGACAATAAAAGTGTTTTGGAGCCCCAGAAATGCCCA
GAAATAAAGGCGTTTCTGCAGACCTTCTGTTCCATTGGTCAAAGAAATG
GTGAGGGGAATAAAAATGGAAGGAAGGAGATCTATGGGATATTACCTGCA
AAGTCTGCAGTGCTTCATCTCCTAGACCAACCCGGACAGTTTCAGCCAAC
CCCATGGTTTAAAAAACAGAGCTGAAATCTGAAGGCAGGGATAATGAATG
AGTTCAACCCGCTCACCATATTTGTTTATGGGAAATGGATATTTATCAAG
GCGAGGGATCTGCCCTGGGGCCATCATCCCAAATTACAGCCAGACTCGGC
CTGCAGGGTGAAGAAAACCTGTTTGGCTGCCCTGATTTTTGTGTATTCTC
CCCTCGGCATCTATTTTTGTCCATTTGGGTACAGCCTATGGGTCCAGGCG
CGCCTCCATCTAACAGGTAATGCGGCTTTAGGTTCTCATGCTCAGCAAAA
GGCACTTTTAGGAAAGGTGAAGCTGGAGGGGTGCAGAGCCGGAGAGCAGC
CCGTCTTACCCCTGAGCACTTCTCAGGAATTACAGCAAAACGTGTAAT
TAAGAGTGGCAAACGGGGTATCGAGTCCTTCGGGTCTCAATTATTTTCTC

FIGURE 10

SUITE 30

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COSMIDE.txt

GAGTGGGAATAACCCGTTGCTCTTCCATCTCTCTGCATTATTCTGCTGCA
GAACGAGTGATGGGCTGCTGGTTTTTACC AAAATACCACCATTTCACCACC
CGAAACCCCTTCTGAGTACCTTGAAGCCTCTTCAGGGTTTTCTTCAGAGCA
CCGTTCTCCATGAGGAATGGCACAGCCTCTCCTCCGGCCCTGGAGAAGC
GCCCCGCTGGCAGCTGGAAGGTCACTTTTCCACACCTGGAGGGGAAATAAA
TGCATTTTCAGGTGGTTGTATCACAGAGCATGCCATCACTTCAGGACAGC
AGAGGCCAGCACACGGCGGCCATCCCCAAAATACCCTTCAGGGCTCGCAG
TTCCCCTGGAGCAGAAGAGCATTTCATTGATGAGCTTTCTCCTCCATGGTC
ACTGCCTGATGCAAAGCTCACAGAACAGCTTTTCAGAGAGGCCACATACC
TGGTGATGGGGCTTTTACATCCTGGGGACAGAAGAGAGAGGGGGAGAG
GAAACTCAGGTGAGTGCATGACCCATTTTGTCTTTAAAGTATGGAATAAT
GAGCTGTTTTGAGTGGGGGTGGACCTCTTGGGTCTTCCAACATGTGCCAA
TTTTGACTTTAAGTCATAGAAAAGTGAATTGTTTACTGGGGATGGATC
TGTTGGGTCTTTCAACACATGGTCCATTTTGTCTTTAAATCATAGAAATA
AAGAATTGTTTGACCAGAGATGGACCTCTGGGGTCTTCTCCACGAGGAA
GGTGAACCACTGAGGAGCATCCATGCACGGCAATGAATCCTGCAGATCC
ACCCCACTGCTGCTCTCCCAACCCAGCCGTGGATTTCCTCTTAAACA
GACCCCATGAGGACCTTCTGCAGTAAGGTGAAAATACTGGGAATACTGAG
ATGAGGATAAAACGGTGGGGGGAAAGAGGAGGCTGCAAACCTCCATCTCC
TCATTGTGGTGGGGGTTTTAGGCTGATGGAACGGCATAAAATGGGAGGAA
AACACCCAATTAAGGCACCATGCAATTGGTGGGGTGGGGAGGACATCCC
TAAAGGACTTTTCCCCTTGAAAAGCTTCCCTGGAGGAATCACTCACCG
ACTGCTGGCTCTTCTCTCCTGTGCTTTTGTATCCAGCGGGGAAATCTCC
TCCGAGTGTGGCGGTGCTTTTCTGCCTCTTCTCAATCTCATTCTTTCAG
GTCTTCCAGCTGCCAGAGCAAGAAGGGCTCTGTGTTTTCTGCCTGGAAT
CTGAGCCCTCCCTACTGGGGCTCAGCTTTCTTCTGATGCAGAAAGTGGAA
AAATAAAGAGCAGTGGGACTGGAAATACCAGGGGGGACTCATGAGTGGCA
TCCCCCACTGGAGGAGCTCAATGGTGAGCTGGAATCCTTGTAAGTTTA
TCCAATGTGGGGGACAGGAGGAAGAAATCAAACCAAAAAGTCATGAACA
GGTGGCTGTGAATTCGGGGCAGAAAGCTGAGGGCCCTAAAAGCACAGGAG
GCAAAAAGGATGGAGAGAAACGACCCCTACTGATGACACATCGCTGCCAG
CAGCTGACACCTACCAGATCCTCCAGGTTTGGGCACTCCAGGGCGCTCTT
CTTCTCGGAGACTTTCTCTCTCCTCCTTTGGAAACCCCTGATATCCCTC
TGAGTTTCTTCCCCAGTGAACCCACAGAACCTGTTGTTTTAGCCCTTG
ATGGGGTTGGGGTTTTCCCTTCTGTTCTTCCAGTCTGGGGTAGAGCT
ATGGGATGGCTGCGTTGAGCCTGCAGGTCTGCTCCTGGTGGCACCCCTTG
CAGGGCGTGTGGGAGCTCTGGGTTTGTCTTTGTCTTTCTCCAGTTCC
TTGTTCCCGGGGAGATGCTGAACAATGTCACTTTGCAGATTTTGTGAGCTT
CCTTTTAGGATCGAGCCATCGGGAGTGGGGTTAGGGGGTGTATATGGGGA
AACCATAAGGAAATAGGGAAGGAGATGCACAGCCGGATCCTTGTTGGGAT
GTGGAGGAGCACAAGTGAGGATCTTGGGATTTGAGTGTCTCTCAGCCC
AGCACTAACACAGAGCACTCACAGCCCTGGCTCTGAGCTCTCGAGGAAAC
ATTTCCAACCATTTCTGCCCCACTGTCTTGTGTTGAGCCCCATGGCCAA
ATACACATGCCTAGAAAATAAAGCCATGCATTACATATGTATTTAATTTT
TGCGTGGCAACCACTGAGACCCAACTGGAGGAGATAACTGCCATTCACTT
GGGCAGGTTTTGCAGGGGTGAACCTGCACTTCCAGCAAACCCCTCCCTGTTGG
GAAGAGCCACAGGGATGGATGGCACTCTGGGAGCTGAAGAAGTGAAGCA
AACTCCCTGCAACCGCTCCCCTGGGGCACAGAGCCTTTTCATCCCAATA
AGGCTCCATCATTGAGCAAATGAGTCAACCGTTGGGCAAACGACTTGC
ATTGCATCCCGAAAAGCATTAAATGCAGAGCCTGGAAAAGTAGCTGGGCT
GGAAACATCTGCATTGCAGATCTATGGAGCAGAATAGACCCTGAACAGAT
CCTTCACCCAAATTCAGCAGGTGGGACCAATGGCAGCGATGCGTGG
GGCTGAGGAAAGATACCAACACATCAAAGAGCAATATGAAATTCAGCT
GTAGGTTTGACCTTTGGAGGTGGTGGGTGGGGCTTTGTATGGGATACC
CACTCATATCC

FEUILLE DE REMPLACEMENT (REGLE 28) CCTCCC

FIGURE 10

SUIITE 31

69/110

COSMIDE.txt

ACCCTCTTTTAGTTCTCTCTTGGTTCTACAATCACCAACCTGTGTGTA
TTTTGGTGCTGCCTGTTCTCTTTGGGCTTTCTCAGAAGAAAATGGGT
TTTGAGGGAATCCATTAGGTGAGTCCTCACCCCAAGCAGCTCTTCTTCA
CTTTGTTGGCCCAAAGCTGACCCAGAGCCATACACCCAAAGCAAACCCAG
AGCCGTACACCCATAATGAGGCAGGAAGTGGAGTGTGCAGAGCACATCTT
TTAATTAAATTAATACTATCAGAAACGTAGGCAGAGACCAGCTCCCCACAC
CAGGCGTTGCTATTTGCAGTGAAAGGCCGCATACCTTTGCAGGACACCCC
AGATCTGCCCCACGATTGATGTCAAATAGATGCATAAATTCCTTCCAAG
TCTTCAGTGCTCTCTGGTGGTTTCCCCACCCTGCAGAGGGACCGCCCCGG
GGCTCCCAATGGGGACAGACACAGGGCAGAGCAGCGGGTCCCCCTGGCAC
ATTGCTCCAAGCAACCACAGCACACATCCCATCAGATGCCCTTTCATAA
AGGACATCTCAAGGACAGATCTTTAGGGGAGATCTAAACCCAAACCAATC
CAAATGGGACATCAGCTGCCCCACTCGTGGACTGCTCCTCTGAGGGGGGAT
TTTGGGTGATCTCTTGCAAGCGAGCCCCCAGCCCTATCTTGAACAAGGGG
AGGACCTTCTCCCCATTGAACAAAGCCCTGGTGTACACCAAGATGGGGGT
GTCATCATCCGAGCTGAAGAATGCCACCCGACCCCTTCGTAGTCCAGGG
AGACCCGAATCCTCCTGGGAAGTGCATTAGACGTAGGTTGGCACGGGGG
GACGTGAGGGAGTGGTAGGCCTCCAGCGCCACAGACACCTCTTTGGGGCT
GAAGCTCATGGGTCCCTTCTCTCATCGAAGCCCGGGCCACCCCGAGG
CCCACACCCCCCTGTCCCACCTCCACCTCCAGAAATGCCTCCCCGAG
GTGAAGCCCTGGCAGCCCAACACGCAGGGCTCGAAGCTGAACCTCTCGGG
GTTCTCGGGGAGGTCTGTGGCACCAGTTGGCCCCGGGCTTGTTCGGT
CTTCAGAGAGATGGAGGTGGGGTGAGCGGTGGTGGGGTCCATGGTGACG
TTGGCTGTGGGACATGAGGGGGAATGGAGGTAGGATTTAGGCTTGGGGG
AGCTGGAGAGGTTCTCTCTCTCTGTCTCTTTCTCTGGGTGCTTTTGA
CATGGGCTGGTGGTGGTGGTGGGTGATGGTGGGCTGGGTGATCTTTGG
GGTCTTTTCCAACCTTTGTGATTCTATGGGGTGTGTGGGGCTCCACCAGC
CTCAGTGTCCCCCAGTAGAGATGTAGGAGAATGGGGAGAGGACAAATTTT
AGGGCAGCATAATGCGGGAGGGACAAAGACATGGGAAGGGGACAGCTTGA
CATTACGGAGGGGAAGGGGAAGCACAAACACTGTTAGGTTTTGCCTTGA
ATCTGTTACTGGCTTTGTAGGACCACAGCATCAGGATGCTGTCCCCATT
CCCTCCCTTCCCTGTGGGACTGCGTTGTTTTTTCCCAAGAAACCACTCC
CCACCCACATCCACCACTGCTGACATACCTGGCTCTTGCAATTGAAACA
TCAGGCTGTCTGAAAAGGAGAACAAATCACTGCATTGGGTTTATGCTTC
AGGAAAAGGGGCTGGGAGATGGGGAAGGGAACCATGGGGGTCTGGGGG
TTCGCAGTGCAAAAGCTCTGGGTTTACTGCAAGAGCCCCACGACCTCCC
AGACCTGGAGGAGACCCCGACCCCATTCAGTACCTTGGCACTTCTGCAGC
GTCAGTCTCACCAGGACGTTCTTCTGAAGGAAGTCCCTCCAACCTTCTTTC
CAGAGTGGGGGAAATCTCTGCTGGAGGGCTGAACCTCATCATCTCACAGC
TGCAAAGAGAGGAGAAGGGTGGGGATGGGGGGACTGTTGCGTTGGTTGGT
TGGCTGTTCATTTTATTCTCAATAGGAGAAGCTATGGGGTGAGGATATTT
GCACAGGGACGAAATCCCTTTCCCCCTGGGATCCCTCTGCCTTGCAGCC
CTCCCCCAGGGTGCCATCCAAAATCAGGGTGACAATAGGAAGGAGCCAT
GTTACCTATTCAAGAGCCTCCTGATGTCTAAAGGTGGGAGGAGAGGGA
GAGATGGATCAGAAGAGGAGACCAAGGGCTGCCCCCTCGTATGGCAATG
CACAGCAAAGACCACCTGCCCACGGTGTGATCCCCCAGCAGCAACAC
AGGGAGCTCCCATGGGGTTGAGTTTGGGTTCTCAGGGTTTGCTCTGTCCC
CCCATTTCCCACCACCCCTTTGGGTTCTCACCAGCAGGAATTTGCTGTCTG
GGCTGCTGGAATTTGCCCTCCATCTCCAGATCAGGGTGTCAAGGTGGGA
CATCTCCTCCATCACCTTCTGTACCGCATCTCTGTACTTTGGTGACGG
CTCTGTCCAGGTCTGCCAGCTGGACCAGCAGGAAGCGCTCCTTCTCCTTC
AGAAATCGCTGCAACTGCTCGAATTCACACACTATCTCTTCCCTTCCCTT
CTTGGTTCTCTCTGTGGGATGAGGGAGAAAGCCAATGGGGTGGGAATAG
AGGCAGGAAGACCCCCCTGGGGTCTCAGGATGCCGTGTTCTGGGGGATA
TCCAACCAAAACCAATGGGGATGTAACCCCAATGCCAATGGGAGCACAAAC

FIGURE 10

SUITE 32

COSMIDE.txt

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ACTAATGCCAATGGGAATTTATCACCAGTGCCAATGGGAACGTAACAACA
GCGCCAATGGGAACGTAACACCAGTGCCAGTGGGAATTTATCACCAGTGC
CAATGGGAACCTTAACATCAAAAAGCCAAAGATCATCTTGCTGGGCATTTG
GGAGCAGCAGGAATTTTTAGGAGTTTTATCCCAAAGCAAAACCAAAGG
AGGGGGTAGGAGATGAGCTCTGTATGAGGGATATTTACAGAGTTTAGGAG
GATCTGCTACGTTATCTCTTTAACACAGGGGTTCTGCGTAACCCAGCT
GATAAACACAGCCTTAGCGCTTTCCAGCCCAGCTGCGAGCCAAAATGC
ATGATCTGCCCCCAAATACACCAAAACAAACAGGACAGGGCGGAGGGGA
AGGCAGACACCTCCCCTGCTGCACCCACCAAATACAAGCCCGTCTTCCA
CCAGTCTTCTGCTTTCCAGGTACTTTTCCCTCTCCTCCTTGAAGCCTG
GAGGCGAGCCTGAATTTCTTCTGCTGCCAAAAGAAGAAAGGCGGAAAGCC
TGTTTTCCCACTTAACTGCTTCTGTGATGAGGAGAGGCTTTGCTAAAG
CCTGGAATCCTCTGCAAGGTGCAGAGCTGGGCAGAGGGAAGCTCTGTGAG
CACGGTGTGCTGCTCTGGAGCTCTGTGCAAGCTGGGAGTATTTGCAGAG
AGAAAAGAGGGGAGAGGGAAGGAAAAACAGAACTTGCTGCAAAACGTAG
AGAAAAACGCTGCAAAAGAGCAACAAAAAATCAGCACTGACAGCTGCGC
AAGGAGGTGTGGAAGGGCAAGATAAGCACTTGGTGAGATTTCCCTCATAA
ACACCCCAAAACGGCGGCCCTGGGGTGTGTTTCTGTATTTAAGAGCCCTC
AGTGGAATGGTTTTTGCAGGGCTGTGGTGAAGAGCAAAGCATCAAAGGA
AGGAGAGGGCAGTAATGTTGCAAAGGGCTGACGGCGGTGGTTGCAAAGAG
GGAGGATGGGGGGGGATGCGCCAAGCAAAGGGTTGCGTGGGTTACCCGC
AGGGATGCACTGCGCCCTTGGCTCCGGGTTTTGGGACCGTACCTTGTA
CCTGGGCCGCTGGTGGGCAGGGAGCACAGCGTGGGAGCGGTGCGCCTGG
GACGCTGCGACTGCGCGCAGATAGGCTCTTGGTCTCTGTGCAAGAGAG
CTTCAGAGCCTCGCGGTGCTGCTTGCACCAACCCGAGGAATGCAAACTCA
GCTGCCGGGCGATGCTGGCGATATTTGCCAGCTCTCTGCTGGGGCGGAAA
TTTTTGTGCAACGCCGTTTTCTGCACTGCGGACAGGGGAAATTTCCCTC
CAGCCCTTCCAGCAGCGGGCGATGCACTCCCGGCAGAAGTTGTGGCCGC
AGGGGATGGAGACGGGATCCTGGAAGTAACCCAGGCAGATGGAGCAGGAG
GCTTCGCTCTGCAGGCTGTCCAAGGGGCTCTGCGTGGCCATGGGCTTCCT
GCTGGGCTCCGATCCGCAGAGGGAATAGGGGACCTTTCCCTCCTTATCTCC
TCGCTGATAGGAAATCCGGCCCCGGAGGCTGAGCCTGAGCCAAACAGG
GCTGGGAGAGCTCAGCCCATAGGGGATGCTGGTGGGAATGGGGGAGCTC
GCGGCTCCCCAGCACGGAGTCACCAAACTGGGGGGATCTGGGGGAAATTC
GGAGGAAAAGTCAGATTTTGTCTCTCCTCGAGCAGCAAAGAGGGCAGGG
GAGGCGATTTTTCCCTTCTGTGCGATCACTGTAAGGAATTTCCAAAGAAA
ACGCATGGAGGTCTGCTTGTGGGATGGAATATAGACGTATATTGGAATA
AATACAGGAAGACGTTGGAACATGGGAAGGCACTGAGATATAAGCGTGCT
GTGTTGGATATGACTCTGCTCGACTAAAGTGAAGGTGGTTTTAATAGCAC
TGCTCAGAGCCAGGCGGGTTTTGGTGTGTTTTGGGGGAATTACGTGGGT
TTGGAATTGGGAAATATGAGACGGAAAAATAAGAATAATGGAAGCGCCCA
ACGTGGGGCTCGAACCACGACCCTGAGATTAAGAGTCTCATGCTCTACC
GACTGAGCTAGCCGGGCTGATGGGCACGCACCCTTCTAAGCAATACTTCA
TGGTGATCCTGCGGAGGGGTGCTAATAATTCTACCTAATTATTTGTAA
TTATCCCGGTAATTATGGGTCTGAGCAATCGCAATCCACGGGGAAAGAG
CTGATGGGGAAGAACCTATCCCTACGGGAATAGCCGGGAACTGCCC
GGCAGTGCTGCAGGGCGGGGGAAGAGGGGAAAAGCAGGAAAAAATGGG
CAAAATGGAACGTTTAAAGTGGAGAAATTAACAGTGAAAAAATGCAGG
AAGCGTAAAGTAAAGGCTGTGTTTCTGCCCCGTTTTGAACCGGGGACCT
TTCGCGTGTGAGGCGAACGTGATAACCACTACACTACAGAAACGCGCTGA
AGGCCGCTTCGCGCACGGAGATGTGAAGGGGCGAATGCCGGGGCTCGGT
GCGGAGTTTGCAGATAGGGGCGGCTCCGGGCCGCTCCCGCGCCGGTTCCG
GTGAGCACAGAGTGCAGCGGGTGACAAAATGAAGGGAATAATGTAAACT
GATGCTCCCGAATCGAGGCTCGAACCAGCATGTCCGACTGACAGCCGCG
CGCTCTACCGA

FIGURE 10

SUITE 33

FEUILLE DE REMPLACEMENT (REGLE 26)

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CCGTAGAGCGCCACCCCGTTGCCTAGTGACAGGAGCGCGCTTCCGGTC
AAGTGATGAGCGGAGGGGGCGTGGCTTGTGTGATAGGACGGAAGTTCC
GGTCAGGTGGTACTGGAAGGGGGCGTGGCTTGCGGCAAAGGGGACGGAA
AGCGGAAGTGCTGCCGTTGGTTGGCGGAGTTGCGACCATAGAAGAACGAC
GGCGGGCGGTGGGAGGGCGGGAGGTAGAGCGGTCCCCGGGGAGAGTGCTGA
GGGGAGCGGCGAGGCCCGAGGAGGGAGCGGAGCTTACGGGGAGTGCGGAG
CCTCGAGGCGGGTCCCAGCGCTTCGCTGTGGGGCAGGAGAAAGGCTTCGG
GGCAGGAGGAAGAGGGCCTCGGGGCGCTCCCATGGAGGCGGTGGGCGACG
ATGGGGCGTCTCGGGGCGGCTGAACCCGGTGGAGACGCTGCAGGAGGAG
GCGATCTGCGCCATCTGCCTGGACTACTTCGTGGAGCGGTGTGATCGG
CTGCGGGCACAACCTTCTGCCGGGTGTGCATCGCGCAGCTGTGGGTGGAG
GAGAGGCTGAGGTGGAGGAGAGCGGCGGGGCCGCGGCTTGGAGGAGGAA
GAGGAAGAGCTGGAGGAAGAGGAGGAAGATGAGCTGGGGGAGGAAGAGCT
GGACGTGGAGCAGGAGGAGGAGGAGGAGGATGGAGGCGGGGAGGAGGAGG
AGGAGGACGACATGTGGAGCGAGGAGGAAGAGGATGGAGAGCTGTGGGAA
GGTACTGGGGGTGGTGGGCTGCCCTGTTGAGTGTCTTTATGGATGA
GTGAGGGAATTGGGTGCACCTCAGTCAGTTTGCAGATGATGCTAAGCTG
GGGGGGTGTACTGATCTGCCTGAGGGTAGGACGGCCCTACGGTGGGGTCT
GGACTGGGCCCGATGGGCTGAGGGCAATGGGGTGGAGTTCAGAAGGACCG
AGTGCCTGGTTCTGCACTGAGGTCAACAACCCCATGCAGCTCTACCTG
GGGTAGAGCGGCTGAAAGCTGTGTGAGGGAAAAGGATTTGGGGGTGAATA
TGAGCCAGCAAGAGGCCAAGAAGGCCCATGGCATCTGGCTTGTATCAGA
AATAGAGCAGCTAGTGGGAGCAGGAAGTGACTGTCACTCTGTACTGGCAC
ACCTCAATGCTGCACCCAGTTCTGGGTCCCCTCTCACTACAAGAAAGACA
TTGAGGCCAGTGAGGATGGTGGGGGTTGACTCAATGATCCCTGAGGTT
TTTTCCAACCTTGATGATTCTGTGATTCTCAGACCCCGTGAAGAGGAGC
TGTGGGATGGAGTGGTGCAGGGAGAACTCTACTTTGGGGACGATGATTAT
GATGAGGATGTGATGGAGGAGGATGTGGAGGAAGAGGAGGAGGAGGAGGA
TGAAGCGCAGAGCCCTCCGCCCCCTGTCTGCTGCCCCCGCTCGCCGCC
TGCAGACCTTCACCTGCCCCCAGTGCCGCAAACCTTTTCCAGAGGAAT
TTCAGACCCAACCTCCAGTTGGCAAACATGGTGCAGATCATCCGGCAGCT
CCACCCGACCCGACGCGCTCGCGCCGCGCCGCGGGCCCTCAGCCTCAG
GGGGTCTGGGGGGAACCCAGGGATCCTGGTGGCAACAGGAGGTGGGGG
TGTCCGAACTGTGCGAGAAGCACCAGGAACCCCTGAAGCTGTTCTGTGA
GGTGGATGAGCAGGCATCTGCGTGGTGTGCAGGGAGTCACGGAGCCACA
AGCATCACAGTGTGTGCCCTGGAGGAAGTCGTGCAGGATTATAAGGTG
GAGTTTGGGGAAGGTCACGGTGGGATAGTGGGTGAGGTGGGGTTTGGGG
AAGGGCTGTGGTGGAGAAGGCGGGGTTGAGGGAAGAGTTATGGGAGAGT
GGAGGCTTGAAGGGAAAGTGAGGTTGGGATCAAGCTAGGTTTCGTCTTGCT
GAGCTGGTTGGGTTGGAGGCGTGGGAGGCTGGGAAACCACACTGCAAT
GAGGAGGTGGAAGGCTCTGGGTACCCATTTCTGCTTAAAAACACCTTCC
CAGCACAGTTCCTCAGAGAAAGCAAAGGGAAGTGGCGTGAAAGTTGGCT
CTGAGGTTCCGTTTTCAGCTCTGCCACCAAATTAGGGACAAAAGAGGCG
ATGACAGAGGGGATGCCCCAGGCAGGGTTTGTGAGTTGTGTTTCTTTC
CCTCAGTACAACTCCAGAGCCATTTGGAGCCACTGAAGAAGAAGCTGGA
CGCGGTGCTGAAGCAGAAGTCGAATGAGCAGGAGAAGATCACAGAGCTGA
GGGTAAGAGCTGAAGGTTTCTGTGCTTCATAGAATCATACAGGAGAACCA
TCAGGGTTGGAAGAGACCACAAAGATCATCAGTTCCAACCATCACCGCTG
CTGGGAGTGTGCCTTGGTGGCTGAGCAAGGAGAGAGAAGCTTGTGCTG
CTCTGAGCTCTCAGGAGGCATCATATTCCCTTTCCTGCAATTATTGGGC
TGTGAGGCTTGGAAACGGTTTCCAGTTGAATTAGAGCTTAATGAGAGC
TTTGTGTGCTCAGTGTTGAGTGGGAATTEGTGGTTTGGGAGCTGGTATT
CCTCATTGTAGTTGAGGATGCTCTACATCTCTAAACCTGTGCAGACTTTG
CTCAGTTCTGTCTGTGGTGCATTGAGGAGATGCGTAAGCTTATGGTGTGT
GGTGAAACTGAGAGAAGCATAGCACAGCAGCCCAAAATGAGCTGATCTC

FIGURE 10

SUITE 34

TCACCTCCCCCTTCTGCAGCAATTCCCCTAATGCTTTTCTCCCTCTGCA
GGAAAAGATGAAGCTGGAAATCAAGGAATTTGAGTCTGATTTTGAGCTGC
TCCACCAGTTCTCTATTGGGGAGCACGTGCTGCTGCTGCACCAGCTGGAG
GAGCGCTACGAGAGCCTGCTGGCCCCGAGAGCAGCAACATCAGCCAGCT
GGAGGAGCAGAGTGCAGCCCTTAGCCGCTTATCACGGAGGCAGAAGATA
AGAGCAAGCAGGACGGGCTACAGCTGCTCAAGGTCTTCTTCCATCCCTTT
CCTTGTCTTTATGGCAAAGCGATAGCACGATGGTGGGAATAATGCTCCAG
AAAGCTTCTGTGTCATGAGAGAGTGCCTTTAGTTGGTGGGCTGGGTGCTT
CTCCACCCCTCCTTGTGGTGGTTTTTGAGGGAAATGCCGGGGGGGGGG
GGGGGGGGGATATGCCCTGAGAGATTTAGGGTCTGTTTTGGTAAGGAAAG
CCTCCAGCAATGTGTGGGCTGTGTCTTTGTTCTGTGGGGAAGGGAATC
ATCCAGGCTCAGTGTGAGTTGTGGCTGATAAGAGGATTTATTGGGAGCA
ACGGTGGGATTGGTATCAGTCATCCCTAATCCTTTCTTCTTTCCCAC
CTTGCTGCCTCCTTCCCACAGGACATCAAGGGCACTTTTATCAGGTGAGT
GACTTTGTTTGCATCTTTTCACTTTGAATAACTTTTCTTTTTTTAATGT
CAAAAAGCATTGAGCTTTTGTTTAAATCCTGTGTGATGGGTACAGTT
GGGGCCTGGTAATGCAGGGGAAAGCTGTGTCCTAACTTTTGGGTGATGGA
AACTTCTGGCTGATGGGGTGCAAATGGGATCTGGGGAACAACTTGGGAAA
AGACTTGGGAACTTGGGAAACAACTCTGGGGCCATTGGGAAAGGGGAAG
GGTGGGGAGGAGATCTCGGCCCTGATTTCTGGAAGCGTGGGTGTGCCCAT
GCAGACCTCATGCTATAGCGAAACTCCTCACTCTGGAGAAACGATTCTCC
CCATCCTGTGAGCAAAATGGGCAGCGCTGGGAGTTCTCAGCCATGCTGGA
CGCACGTGGCTCTACCCAGCTCTGTCTGCTGGCTGAGGGAGGGTGGGGG
AGGCTGGCTGCACCACTGCAACCACTTTGGCCGATCCATGCGTTGCTCTG
GTTTTTCCAGAGCTGCATGCAGGCCGCTCACTTCTTTTCTGCTGCTGAA
ATTCTCTGCTTTCTCCTTTCCCCCACCACAAAAGATGTGAGAACATC
AAATTCAGGAGCCCGAGATGGTGTGCTGGTGGACGTGGGGAAGAAATACCG
CAACTATTTCTGCAGGATGTGGTGTGAGAAAGATGGAGAAAGCCTTCA
GCAAAGTTCCACAGGGTGAGAGAGTCTCTTCTTCTACGTGGGATGGGG
TTCCCTCCACTTGGGATGGGATTTCTCCAGCTCTCTTGGGGTTCTCCTTC
CATCTCTGTGCTCCCATGGTTTGCAGCCTGATGATCCTTTAGGAAAAGCA
GCATCCCTCTGTCTCTCTGTGCTTTTCCCTTTGCTTGTCTGGGTTT
TCCCTATTGTAGCTCCTCCATAGAACTGGGGTTGATGTGGATCTGGATT
CATTATAAAGGAGGGATGACTGCCTCAAACTCAGCATGGTGCAGATACGC
AACCAGATGAGGATTTAGGACTGGGGTGCAAGGGGGAAAAAAGTGCCAGG
TGACCCCTAAGCAACGCCCGCTCTCTGCCCTTCCCTCCAGCTGACATCAC
GCTGGACCCGGACACCGCTCACCCCTCGCTCAGCCTCTCCCTGGACCGCC
GCAGCGTTAAGCTGGGAGAACGACGCCAGGAGCTCCCAACAACCCCAA
CGCTTCGACTCCGATTACTGCGTCTGGGCTCCAGGGTTTACCACAGG
CCGTCACTACTGGGAGGTAGAAAGTCGGGGGCAAGAAAGTTGGGCGGTGG
GGGCTGCACGCGAGACGGCTCGACGCAAGAAAAAACCATGGGGCCTCAT
CAAAAAAGGGAGATCTGGTGTGTTGGCACCAATGGGAAGAAAGTACCAAGC
GCTGACGGCCATGGAGCAGATGGCTTTGTACCCAGCGAGCGGCCCCGGC
GCTTCGGTGTCTACCTGGAATATGAACGGGGTCAGCTTTGCTTCTACAAC
GCTGAGAGCATGACCCACATCCACACCTTCAACGCTTCTTCCACGAGCG
CATCTTCCCCTTTTCCGAATCCTGGCTAAGGGCACTCGTATCAAAATCT
GCACCTGATGGCCCTCCAGCTTCTGATTTTTTTTTTCCCTTTTTCCCCC
TGCCTCATCCTTTGGGTCCCACTTTGGGACCAGACGCTGCACTTGTGTGTC
TGCACCTGCTTGTCTCACAAGGCCTCTTCCCTCCTCTCTCCTGTCCCAGC
CTCTGTCCACGTCCCAACTCTTCTCCGGGGTCCGATCCAGGCTGGTTT
GGTTTGGAGAAGGGATCCAATCTCCTTGTGAGGTTTTTCCCTTCAGCTC
TTGGTGTATGGGCTCCCTCTGCTTTCCTCCTCGCAGCAGCTTTC
CAGTGTGCTCTTCCCCGTTTTGTTTAAAGCCTGTGGTTCGAGCTTTCGCTT
GTTTGGCCTCTTGGATGCAGAGCTCGAGCTGAGGATGCTGGGGTCTGTA
CATTGTGACACGAGCACTGCTTGTGCCCTCTTGGCCATTGCTTTCTGAAA

FIGURE 10

SUIITE 35

COSMIDE.txt 73/110

GTCACCTCAGATGCACCAAGGAGCCTCATTCTTTTTTATTTTTCAGTTCTG
GGGCACAACCCTCTGCCCACCTCCCACCCAGCCACCATCTGGACCTCAAA
CCTTCCACGTTCTCCTATTCTGCCACTTGTCCACCTTCCCCTTTTGCTCT
TCTTCCCCCTCTGGGGGTCTCCAGCTCTCCCTCTGCCCCATCATTCCCTC
GCCAACCATTTCTTGTGGGCCTGGCACTTTATTTAGGGCCACGTAGGCCG
GGGAGGGTGCAAAAATTGGGCAACTTCCACCTCTGAGGCTGCTCAGAGT
GCAGCATCGCACCAGGCCGACCCGGTGGGAAGCAGCCTTGTTCCTTGT
CAGCTTAAGAGCTCTCTGAGGTGGGGGTATTTATTTTCTCTTCCCTTTTC
TCAGCTGCTGTTGAATTTCCAGCTGAATCCTGTCCCACCAGAGAGACTCT
GATTGCACCCTGTTGTGTTTTACTTCTTTTGTGGTGGATTGGTATTTT
TTTTTTCTGTTGGCGTTACAGAGCTAGTTCAAATATTTTTGGCTAAAAAT
AAGAATTAATGGAGATCTAGTTTTTTGAAATGTCAAGAAATAATAATAA
TAATAATAAAGAATAAAGAATAAAGTTTTAAAGCTGAGCCTCTCCCTTAT
TGAGAGCCCCCAGGGGACAGGAGTTGTGGTGCAGGCCCCCAGTCTGCTG
TTAACTCCTGCTGGTAAGATGTGACTTAAGCCTTGCATCGTTAATCTTAA
CTTAATTAGCAGTAATTTGGATTGGGCTGCTTCCCTTCAGCAGCTTGTA
AGGGATAGAGGCTGCTGGGTGAAGTGAAGTCTGTGTTACCACCTCTCCTG
CTCTCCCCACATGTTTTTGGTGGTGGTGGTGGTCTTTTTTGGCCACGGC
TCTATCTCCCCAGGTGTGCACTCACTGTGGGCTGCTACTGCTCCTGAAAG
GGCTCAGGGAGACATTTGAGTCCCTTCGTCCACACGTGGGAGGAGAGCAC
TGATGTCCCCATCCTTAAAGTTGTGGGCACAGCCTTGGTGGCAAATCCAG
AATGGGATATAATGCAGCCATGAGCTCAACAGAGCGCTCTTTTATTGAGT
TTTGTGCATAAAATCTGTGTGTTGTTACCACATCCTCATCTGGTTCCAAT
GGTGACTTGCCACACCCGGACGAGGTTATCTGTGTAGCCAGCAAACAGCG
TCTGGGGAGAGAAATGGAGGAAGTGGATCATGAAAAGATAGGAATCAGGC
CTCGGTGTGAACGTAAAAATCTCAGAAGGCAGCTCCCAAAGCGGAGGTGC
TGGAGGAAGGTGGGAGTTTTAAGGCTGCAGGAGGAGCAGTGAAAAGGGAA
AGGAGAAGGGGATATTTCTACCTGCCCATCTGCAGACCAGCCAGAGAGG
TACACTGGGGAGGCTCAGCTTTGCTGCTGGTGTGATCACCTCCTGCTTC
AGCTCATCCACAATGATTTTGCCTTCCAGGTCTGTGCAGGACAGAAGAG
AGCGTGAGGGACTAAGGTCTCTGCAGGGAGACTGCTGTAGCCAAACCCCAAC
CATTCCAAATCAGAACAGGCTCAGGGTGTCTCAGAAACAGCCTCTGGGTTT
CCGACAGGGATGCAGTCAGATGGCATCGAAGTTTCATCACAGCAGAGTG
GTGGCTGTGCCCCACACCACCTCCAGTCCAGGGGATGACAGTGCCACC
AGCATGACCCATCCACGTAACCAAAGGGCTCTGCACCAAGGCATCTGT
GGGGCAGGGCGAGGATTTGACCACTCTGCCTCCAAACCCACAGGAT
AAGGGAAGTGATTCTTAGGAGGTAAATAGGGATGTACATACCCAGATC
TTGATGCTGGGGCCGGTGGCAGCGCAGAGCCAGTAGCGGTTGGGGCTGAA
GCACAGCGCATTTGATGATGTCCCCTCCATCCAGCGTGTACAGGTGCTTGC
CTTCATTACAGTCCCACAGCATGGCCTGGCCGTCTGGGGGGCAGCAAAG
AGGAATCACAGCAAACCATCAAACCTGTGGCTTTGTTCCAGTTGTCCATC
TAAAACCTTCCAGCTTGGAAACAGCACTTGATTTGACTGAGATGTGGG
TGAGTTGCCACAGGACAGCAAGAGGCACATAACTGAGCTGTGAGAACAA
AGAATAAGCTGCAATTTGGCCTCAGCTTTCCCCCAGGGTGTACCTTGCT
CCAGAAGCACAGAGGGAGCCATCAGGGGAGACAGTCACTGTGTTCAGATA
TCCCGTGTGGCCGATGTGGTTTGTCTTCAGTTTGCAGTTAGCCAAGTTCC
AAACCTAAATGAGGGTAAACGTGACAGGCTCAGAAATATGGAGGAGAAAA
AAAACAACCCTCTCATGATCACTGCTCAAATATTCCCCAGAACGCCGCAC
AAACCCCAAAGGAGCTGCTCCTCTCACCTTCACCAGCTTGTCCCAGCCAC
AGGAGACAATGATGGGGTTGCTGCTGTGGGGGAGAAGCGCACACAGGAA
ACCCACTCAGAGTGGCTCTCGTCTGAGGAGAGGAACAGCATTGGGTTGA
AAGCAATGAAAAGCATCCCCAGTCCGAGCTGCTGCATCCCACTGCTCCCT
GAGCCCCCTCATAATTGCAGGACGTGTCTCAGACCCCCCCCCAGAAAGAAA
GGTCAGCAGGCACTGTGTCACTTCTAATCATTAGGACGGAGCTGGGAGAT
GTGGATTACGGAT

FIGURE 10

SUITE 36

COSMIDE.txt

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ACTCAGAAACAAGCAGAAAGAGGTTTATTTTACACAGTGTGGAAACTCAGA
TCCGTTGCCTCACCTGCACCGTGTATTTGCAGACACCCAAAGTGTTCAG
AGTTTGATGGTTTTTGTCCCTGGAGCCCGAAACGATCTGGCGTTGTTCGA
GGAGAAGGCGACGCTCAGCACATCCTTGGTGTGGCCAACAAGCGGCGGG
TGGTGGTTCTCTGCAGGGACACCAGGAGGGTGCACGGGAGGGACAAAG
CTCAGCAAACCCCATTAATAATTAACCCTCCCCTAAATTGAGGAGAT
CGTGCTGCAGTGCATAAATTCTTAATGAACACAACCTGATGGAAGCAGGAA
GGAAGCTAAAACGGAGTCATCTCCACATGGGTTGAGGAGTGGTGGTTCCT
TCCCTCCTTCCGAACAGGAACAAAAGGGTGCCAAAGCTTTTGATATAGGG
TTGGAATAATCATGAGGAGTTTAGGATATAAACTCAGCTTCCGTGGACA
CACAGCAGCGTAAGTGCTGAACGCTTTTGAGGAGTTGGGGTAGTTCTGCT
TCCTGAGGAGTTTCTTCTCCTATAGTACTCCCAAAAATCACAGTGCAAGA
AGAGCCGGTGCTGCTCCAACCTCACCCCAAACCTCTGTACCCCAAAATCAC
ACCGAAGGAAAAGCCTGCTTGCTCCAGTCTGTACCCACAGCGATGGTGA
AGGAAGAACCAAATCCCCCCTGCTGCTCCACCTGCTTCTCTCCCATCAT
AATTGCAGGACGTGCTCCTCAGATCCCGGAGGATCAGCAGACTGTGTGAGG
TGTAATCACTGGGAGAGTGAGCTGAGGGAGGAACCGCTTTGGTCTCCT
CCAAGCATGATTTACCACCCAACTGAGAGGAACCTCACCTCATTTTCACG
CTGTACCGCACACCTCTCACCCACCCCAACACCCAAACAAAACACAGAGC
CCAGCTCTGCCCCAAACCCCAACCCCAAGCCCTTTCAGTCCCCAGGACT
CAGCTGGTGAGGTCACAGCCTCAAGGTGCCATCCCAGGAGCCCGACAG
CGCAAACCTGCCATCGGAGGAGATGACCACATCGCTGACAAAGTGCGAGT
GGCCGCGCAGGGCGCGCTGCGGGATCCCGTAGTTGGTCTCATCTCGGGTC
AGCTTCCACATGATGATGGTTTTGTCTGGGAAGGGGGAAAGGCAGCGGCC
TCAGCTCCAACCCCTTCTCACATTCCTCGTCTCACTGGGCTTTATCTCCT
CATAGCAATGGGGGGGTACACAGAAGCACCGCACCCCTTCTCTCAGCC
CCCCAACCGCCTCCCTACGTCTCATACACAGCAGCCTCCCCACCCTGCA
GCTCTCTGTCCCCGAGCCCTGCACCCCATTCATCACCTCCCTCCCCCAT
GGTCCCCCGCAGCCCCCTCCTTACCCTGACGGTCTCCCTTATCTCCT
ACAGTCCCTCCATAGGCCCCACAGTTCCTTCCCCCCCCCCCCACCCACAG
TTCCGCCCCCCCCCGCTCGGACGAGGCCCGAACCCTCAGGCGCGGCCCT
CACCCCGCGACGCGGAGAGAATCATGTCCGGGAACCTGCGGGGTGGTGGCG
ATCTGCGTCACCCACCCATTGTGGCCCTTCAGGGTACCGCGGAGGGTCAT
CTGCTCCGTATGGCGGCGCGGGGCGGAGGGATGGCGGCGGATTCAATA
AAGGGCCCGGCGCGGTCCGGTCTACCGCCCGCGATGGCCGCCAGCGCGG
AAGAGAAAGAGGGAGGTGACTTCCGGCGGAAGCGGAAGTAGCCGCTGGG
TTGTACGGCAAGAGGGGCAACATGGCGGCGCGCATAGAGAGCAGCTGAA
TGGGGGAATGGGCTTTGGAGGTGGGGAGGGAAGGTTGTTCTCTGCCGCTG
CAGGGACACGAGGTGCGGGCAGAGCACCTTCTTAAACATTGCTATTATT
TAACGTTTTTACATTTAGCATTTTTATTATCCCTGTTGTGCCAGGACGGAG
AAGAGCAGGGTGTGCAGCCTGTGCTTATCACCTGCAGCTGTCCCTGCACC
CCACAGCCAACCAAGTTTGTGACGCCTGAGCAGGATCTGACCCAGGAAG
GCAACAGAAGGTCTGAGTCCTCCTCCCTTTCTTTTCCCATCCCTCCAC
GCTGCAGTTTGGGGGCTGTGACCCGTCCGCTTGTCTCAGTGCTCATTCGG
ATGAGCAGTGTGATGGTGATGTTTACAAAGTTTTTGGCATCCCTGTGGG
TTCCACCCCGTTTTTGTCTCACCAGCCTTTTCTATCCGTCTTATCAGC
AGATCATCCTTGTATTAGATCTGTCTTTTCCAGTCACGGCTTTGCATT
TTCACCTTGGTTTTTACCACCTAACATCAAGCCTTTTGTCCCCATCTGATG
ATATTTCATGCAGATAAATCCGTAAAGCAGGGAAGAATTAAATTCTGGCC
CTTCTACACCCATTTAGGTTTAGATCTTTGCAGCATTAGCCAAGACGTG
CTTCCAGAGCCAGGAATAACGTGTCTTGATGTGCCAACACACCTTGAAAT
CCAGAAAATTGCCCCAAATAGGCATGACTCAGCAAGCACCGTAGTGGGC
ATGATTTGTTGGGTGACCCGTGGGTAAAGGAGCCATTGTTGGACACCA
CGATGTCGTTTTTACAGCCCTGTGAGCGCAGCGTCTTAAATTGCCCTCC
AGACATTCCAAATTTGAGACCTTAATGCCAAAGGTGAAAGGCGTCA

FIGURE 10

SUIITE 37

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COSMIDE.txt

GCCCTCCGGGATGAAGGAATCTCTGCCGGGGTTTTCCGTTGGATCACAGC
AGGAGGATTTGCTTTCCTAAAGCATTAGAGTGACGTGGAGAGCCCAAATC
GGACCCAGTGGCCACATTCTCCCAAGGAAAACCCTTCGGGTGCCCTAC
GGTTCCTTTTCTAGCATGATAACAACTTCTTTTTCCATCCGCCCATCCCC
TTTTGGGTTTGGAGGTTGACAAATCCCCACTGAAATTCCTATGTTGCACA
CATGTCCTTCATTCTTTAAGTAGGAGTTAGCAAAGGTTCCGCATTGACTT
AATTCAGAGCGAGATCAACAATTTTAGGCATTCTTTATGAACTTCACATT
GTTTTATGCTGATCAGCAGCAAAAAACATACAGGAATAGGAGTGTGTCT
GTAGGAGTGCTCTGCATTTTCTTGCTCGTTTGGCTGATTAAGGAAGCTGG
GAGGAATGTTGTGAAATAATCCCAAGTGATGAGAGACTGTGGGTATGGG
AGGAGATGCCCTCTGTCTGGTGAGCAGTAGGGACAGAAGACCTGAGCTC
ATTCATATATCTGTATATTAAGGCAATGCTAACCAAGTGCTGTCTGTGTTA
TTTGGGGCCAGGAGTGGCTTCTGCCCGTTGGTGCCCATAAACAGTGCT
GCCCCATTTGGGATTGGGGTCTGCTCGCAGACCACATCCACCAACCAACC
CATGGCTGATAGCAGAGAGGCGACCAGGTCAACCCTCCATATATCTCTGC
AGAAACCTGTTCTGTCTATACAGGGATCCCCATCCCTCCCCAGCCCTC
CTTCCATCCTCGGCATTTGGGTGGCTATAATTAGGCTCTGGGAACGTTT
CCCTGCTGCCAGCACAGCTGTCTGTCTGCAATGATCCTTCCAGCTCTCT
GCGGACACGCAAACCCTCCAGCAATCCTAAATACCCATTTCTGCACTCC
TGGGACAAACTGGGAGCTGCCAAAAATCTCCAGCCCCCACAGACGTGAC
CATCACAGACCAAGGAGCAGAGCAAGCGCAACGTGATTACGGTGCAGGT
CGGGGTAAGCCTTTCTCTTTCTTCCACAGCCCAGGATTTGGGGGATCCT
ATTGGCTCTATGGGATCTGGGAGATGCAGGAGAAATGTGATCCCTTTGCT
GTAGCAAAACAACCTTTTAGAGTCTGCACCTGAATCTGGCAGTACTGGA
AAGCAGGAGAGGGATTAAGAGTCTTCTGCATTATCCTGCTCATAGGGAA
ATACAGCACAGAAATCATTGGGGCTGCTTCTTTGCTTTCTTGGCACAAA
TTTAGGTCTCATTACAGCGTTTCTTTGACTGAGACCCCAATAGGATCTA
CAGGGGTAGAACAAAGCAGACAAAAAGTGATTGATGTTTCTATGCGATT
TGTTGCCTTTTCCATTGAGATTTCTGCTTTTCTATGGGGCTTTTGGCT
TTTTACAGCTTTTTTTTATTCACTGTAGTGAATAGAAATTTTAGGGCTT
TTAGGTCAATGATGCTGTTATGAACACAGAGATGAACTCATAACACCTTC
CTGGTGTGGTTTGTCTATGGGATAGAAAGGAGCTCATGGTGTCTGTGGACA
ACTAACAGAGGTGCCTGAGGGCTGGGGCCCTCTTTGTGCCCTTCTGGGG
TCAGCAAACTCCTTTTATTAGATATAAATCCCTCATCCACAATTTTAC
CAGTCTTCCCAATGCAGACCCCAAAAAACATCCCAATGACAAAGTCCAC
GAAGTGAAGAAAAGCAGCAAAAAGCCTCCAGCCCCAAATATTTATCCCTT
ATCCCATTTTATTCTATGGGGCAAAGCTATTCTAGGCATCAGGAAGGTGG
AGATTCCAGGTCAGTTTGTTCCTAATTGTGATCTTTTAATGATGTTTCTC
CCATCAGGTGGACATTTGGAAGTGGTTCTGACTGGGAAGAGGACGTGATG
ATGGCATCAGGTAGAGCTCAGAAAGTGGTATTATCAGCAAAGCAATTTT
CCAGGTCTGTTTTTCCATTTTTTCCATATTTTTTCTTATTACAGGGAA
GAGGAACGCGGATCTTGGTGAGTGATTTTCTTCTTTTACCTTCAAAAAG
TCCCTTTCCATGTGTAGAAATGGATATACGTACCCCCCACTGATACCCAT
TTCCTTTGTTCTGTCTTATATTTATACTTCCCATATTTTGAACACATG
AAAACAAAGCCACATTAAATAAATTCATAACAGTGCAATTTTGGACT
ATTATTTTCCATAGAAAAGTATTAATCAGTGCAAGTGCCTCTGGAGG
TGACTTCTGCAGCACCCAAAGAGAGAGGCGTAGGGCTGAGTGCTCTCTCT
GTCTCTCTTTTAGAAGAATGGGATGCAAAAATCAGTGAGTGCCCTTTTTT
CCTCTCCCTTACGGTGAGGTATGGGTGTGGAGGACCTGAATTAATGTGA
ATTCTCTGTTTTAAGGGAAGCTAACAGAAGATTTTGGTAAGTCGCTTAT
TTTCTCGATCTGAGTGATATTTCTACACCTTTACCATCAGTGATGACC
AACGTGTGTATGCATTTCTCTTTATTCCATTTAGAAGAGAGCGACACAGA
GCTCGGTGAGTGCTTTGGGGTCTTATCAAGGTGGAAAGATGCCCTCTGT
GCAACAGTGGGGATTGGGAGAAGCCCTTCAGCTCTTCCATTTATCCACAT
CTGATACCCAGATGGAGTCAGGATGCAGAACTGGAGGAGGAGGCCAAAG

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUITE 38

FEUILLE DE REMPLACEMENT (REGLE 26)

SUITE 39

TTGCTCTAGGACGGTCTGAAAAGTGACCAAAATCTGCTTTTACTCATTTT
TCTTCTTATTTTTTTGTAGCAAAGTGCGATGCAACGATCAGTAAGTGCTG
CTGCATGTGGGGGTACCTCCATCTTCGGGTCAATTTCTGCTGTTTCAGCA
TTGAAAGGACATCAGAATTCCTTAAATCCAACAAAATTTGGGGTCACTCGA
AGGAATCTTTCAGATATGGGGGAAATCAGAGCCAAATTTTGAGGGGGGG
AGGGAAAATCTCAGGGGTGTTTACAGTGAACCTCGGTGAGTCCGTTTCCTTT
TTCTGCTCTCAGGACTGTTTACAGTGAACCTCGGTGAGTCCGTTTCCTTT
TTGTTTTTTTTTTCTAATTATTATTTATTAGTAGTATTATAAATCAATAT
TACTGTTGCTTATACATATTGTTGTACATTATATACATAATACATACATT
ATATACAGTATATAGTATACAGTAGTATATAATATTATGTATTATATATA
TATAATGTATTATAAATGTATATCTAATATATGTCTGTATTAGATAT
AATGCATATATATTATTGTACTACAGTCATATTATAATACATTACTTAT
ATCTGCCCTTTTCCACACGTTTCATTGACCTGATTAAAACTAAATCCTA
AAGGCAGAAGAAGATGAAAACCCCCAAATTAACACCAAATAATTGCAGCT
ATAGATCATATCTATCAAAGCAAATTTGCCTTCAGTCCACATCACGAAAT
TAACAATAGAAAGGTTTAAATTTGGAACGTACAAACAATGACAAATAACC
CCCAATGGCTTTTCTCTTCTTGCAGGAGAGCGTCACACCAAATAGGTAC
GTGAGGTGTTTGCTACCTTCGTTTGAAGGAAGAAATTGCATTAATAAAA
CCTCTGTCCAATATGAAGCCGGGGTCAAATTACTCATAAATCACCCTGA
TTGTCCATGAATTAACAGGGAAAAAAGGCTAAACTTGAAAATAACATTT
TTTTCATCTCTCTTTTAAGGGGAACCTCACTGCAGAAGTTGGTAAGTCTCT
TTCCCATCAGTTTAAGCAAAAATGGTTCATCAGATATATAATAATCCCTT
ATTTCTGCTTGTTTTAGGGGACTACAACAGGAACTTCGTAAGTGCCTT
TAACCTTCTCCATTAAGAGTTAAACCTTTCAATATTTTGTATGCTTCAAT
TGCTGAAGCCACCAAAAATGTGTTTTAATTGTAAAGGGGCTGAGCGTCA
AACCTGAACACTGCCATGTTGGGGGCTGAGATTTCGTGGGATTTGGGTTTT
CAGTGTGAAAATGCCTCTGGGTTTCTGTGCCTGAGCTCAGGGAAACACGA
CCAGGGCTTCCAGTAGGAATGAGACCCCAAAATATTTCTACCTGGGGCC
TTTTCCCATTTGGGAATTTATCTGTAAATCCATATTTCTCCACGTTTGAG
CGTCACTCATCAAATGTCACAATCTTGGCAATGTTGAGAAGATATATAGA
TATCTATTTTAATACTGATTAATATGGAGGTGTTTGTGTTGGTCAGTGAT
GTCATCGGGAAAAGATCTGAGTCATTGAATCCCCATTTCTTTCTCTTTA
TTTTAAGGGAAACACGCAGCAGCAACTTGGTAAGGGAATCCCTCCCTGGG
TTTGTTCTCTTGTTTTCTCTTTTGGAGGGGGATTTTTCTATGTCTTCT
TTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTT
CTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTC
TTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATG
TCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTA
TGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCT
TATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTTTCTTTCTTT
CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT
ATCACCTCAAATGAGCCTGAATGTTTGCAGTGAAGGACTGAGCACAGCTG
GGCACTAATTCATCTTTATTTCTCTTATTTACAGAGGAACGCGATCTG
AAAATCAGTAAGTGCTGCCCCAAAGCCATAGGGCTATGCTGGGCTTCATC
CCCACAACATGAATTTTATAAATTAAATAAATAAATAAATAAATAATTTT
ATATTTTATGTATTTGATATTAGCAGTATTTAAAAAAGAATAAATAA
CTCAAGAATCTTAGGATCAATAGTAACACAATGATGCAACGTGGATACAA
AAGCAGTAATTCCTATTTCTTTGGGTTTTATCCTTCCAGGGGAACACGA
AGCAGAGATACGTGAGTGTTATTTTATATACTCTATAATGGAAAACCTTT
TTCTCTGTAATATAAATAAGGCTTTATTATTTGAGGGGTTTTTTGGCTT
AACGCAAATGCGAAGTGCTTGAATTCTACGTATGAAATAGAGGATTTCC
CATAGAGAAAATGCAATTTGGGGCTGGAATAAAGTTTCATTTCTTG
CTGAAAAGTGAATGAAAAGGGGGGAAAAGAACATAAATAATGAGTTTTT
TCCCTCATTAATCTGTATGAAATGGGTTGGGTTCTGAATGGTGATGTC
AACACCTCGTTTTGGGTTTCAGCCCAACATAATATGTGTCTGTCCTTTATT

FIGURE 10

SUIITE 40

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COSMIDE.txt

TCTGTATCACTGGTGTAAAGAGAGCTGTTTTGAACTAATATCTCTTTTT
TAATTACTTTTTCTTTTTCTTTTTCTTTCTTTTTCTCCCGTTTCTCTC
TGTTTTGCTTTAAGGGCGCCTCACTGAGCTGCTCGGTAAAGTGCATTTCTC
TCCTTGCACTGTCAATCCAGCAACAACCAAAGCCTATTTGGGGGGGA
AGGAGGGGATAAAACACAATAATGATGAAATCAGTGCTTTGGAAAGGGTG
CAATTATTATTTCTCTGCAAATGAATACTTCTTTTTCCCTTTTGTGTC
AGAGGACCGCGATTCCGATGTCCGTAAGTCCTTTTGTGTTGCCGGAGCT
GTGAATCCTCCAATGGGAAATGCAGAATTTAGAGTCTGCCCCAAAAATG
ACCTTTTTGAGGCTACAAGGGATGGGAAAATAAGGAGAAATGTCTTATT
TATTGATCTCCTTGTGTTATGTGCAAACTGGGTGACTCTTCTCTGCCGAA
CACGTTAGAAATAAGAACAACAAATGGGAGGAAATGGTATTTATTCATAT
CTGTTGTTTTCTGTTAATTTTTAGGAGAACAGGACATCCTCATTAGTA
AGTGGCACTTTGGATTGATAAGAAATGCAGCTCCTGGGGACGTTTGGGTG
CTGCGATTGCTGGCACTGCTGGGGCTTTGTGTTGTGGTGAAGTGAATT
ACTTCAAAAAGAAGAGAAGAATGGAATTATCTGGAGAAAAAGGGGAATAAA
TGGAAGTGTGTTGGGAAAAGAAGGAGGAATAGAATGGAATATTGGGGAAA
AAAGTGAATAGAATGGAATTATTTCAAAAAAATGGAATGAAATTTAGG
GAGGGGGAAGGGGAAGTGAATGGAATTATTTGGGGGAGAAAAAGGGGAA
AATTGAATGACTGGGGGGGGAATGGGGAAATAGGATGGGAGTATTTTAAA
AATACAGAATTGTGAAGGTTTCAGCCCATCTCAGAGAGTTTGGTATCCTC
GAGTTCCTTTCTTTGCAACCCATTGAGCATCCTTGGGATGACACCAAATTC
TGTTTTCTCCTTTCAAGGGAACCTGTGAGAAGAGCTCGGTGAGTTATTT
CCAATTCTTACATACAAAACCTGATTCTGGATATCTTTTTGTGTGTTTT
CTGCTTTGCCTCTTTGTGTTTTAAGAGGCAACTGCAGAAGGAATGGCACA
AAGGGTGCAGAGGATCTTTGGGATAAATAACAGGGAAAACAGGGATGGGA
TAGCAATGAGTTGGTGAATAATCTATGGCACAAGGTGACGGCGTGTT
TCACATTTTGCTTTTTCTCTCCTTTTAGAGGAATTAAGGGGTGCGGAAG
TTGGTAAGTGAGATTCCTTTCCCTCTTCTCCCCAAAAGGATAAGGGGTAA
TTTGGATTCTGATCTCTTTTCTCCTTTTTGTTCTTAGAGGAGAGTGTT
CTGGAGAGGGGTGAGTATCATTCTTTCTACTGCTGCTTTTGAAGTGAAG
GAATCCCCCATAAGCATGCTGGTGGGATGGGAATTCTACATCTGATACAC
AATTATTATCATTCTTTCATTTTTTATACACAGAAATAGATAATTTTTTT
CCTTTCTTTTCTTTTTCCCCCTTTTTTAGAGGAACATGATGCCAGAATT
GGTACGTGTCCATCTCCCCCTGCTTTTGTGGTGTCTTCAAGAAGGCCAAT
GGGGTCATTTGGGATTGTTTGGGTGAGGATTGGGTTCTTGATTGAATTT
GGGGGAGGATTAGGTGCCCCAACACATCAGGTCCCATCTCATGTTT
TCCTATGGGCTTGATCCTTCTGTTGGATACCTAAGAATACCTGAAATCC
ATAATATGCCATTAGAAGTAACACATCCATCAATGATATATCCATAGAAT
ACAAGAGAACGGTCTACATTTACTTCAGATCCCATTTTCAAGTTAACCAT
GAAAAAATACCCAAAGACTGAATGTCACCATTCAAGGATCCCGTGTGA
AAATCATGACTTCTGCTTTAATTATAAGAAAAATGAAATTCAGTGTTTTT
ATTCTCTTTTAAGATGAAGTCTCAACAGAAGTTGGTGAGTATTTTCTGC
CCTCCAGCAAAACCAAAGCATGCAGTTTGCAGTCTGTTTTGGATATATAT
TGACGTGGATATATAACCTGTATGTTATAACACCTCTGGTTTCCTTTTC
TCCTTCTTTTCTCAGAAAAACGAGAGAGAAGAATTGGTGAGTATCAAAC
TTCCCCCAGAAGTGGACTTTGGTGTGTTGGGAAGATCCATACCACCAG
TTGGTGCCAACTTAATGGAAATCCTTTGTTTTTCTTTATGTTTTCAGA
TGAAGTCACTGCAGAGCTCGGTAAGTCGTGATTATAACTCATAACGAGTT
ATAATGCTATTGTTATATATAATATACATATTATATATTGTTGCTATAAT
TCATAATAGAGCAACAATCACAAGGCACAGAAATATGGGTTTGCTTTGA
GAGCCAAACCTTAGGAAGTGATAACACAATGGGAAGAGGACAATGACCAT
TTCTGTGTTCTCTTTTTCAGAGCACTACAAGGCAAAAGCAAGTGAGTGT
CTCCTTCTCATCTTCAGCACGTGAGAGATTTTGGGGGCTTTTGGGACGG
CTATGGGGATTACACATAATAAACAGAAGATGAGAAGACAGTTTGTGA
ACTTGAATTCAACTGGTTTCAATTTGCTCAATTTAGAGTATTAATAATC

FIGURE 10

SUITE 41

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COSMIDE.txt

TCCCCAGTACCCAATTATACAATGGGATTAATTACAGCCTGCCAGGAAA
GGAGCACTGAATTTTTTCTGCGTCCATCCAGCATGAAGTCCATCAGACT
TAAGCTTACAGCTTAAAGAATGGTTCATTTTTTTCATTTAACCCCTCGT
AAGTTAAAGATGGAATTCAGCATCACAGAAGTAGCCAGAAATAGTCAA
AAAATGGGTCATGAATTTCCAGAGCACCCCCCACACTTTCCTTGGTGAA
TAGGAAAACAAATATTAATACTAATTAATTGGTTTTTTTTTCTTTTTAGG
AAGATGTTTTGAGGAACACAGTAAGTGCCCTTTTCTCCCTCTTTAAGCA
TCACTTTTCACTTTAAGTCTGCATCACAGTTAATAATCCATCTCCTTATT
ATGCATTTTTAGGGAGAGGCGAAGAAAAGTTGGGTAAAGTCATTTGGTTAA
TTGGGTTTTCTGCTTGACAGCCCCATCCAGGAGCTCATGTCCTCCTCTTAG
TGCTGCACTGTAGAAATATCCAGGTTAGACGTGTAGGTAGGAAATACTG
GACCTGCGTGGAGGTATTGACAGCCCCATTTATGTGTAGGGGAAGCAGAA
CATCAAATATTGAGCCTTGAGCTCCACGAAGACAAGCCACCTCTTAGA
TTTCAAGCGAAGTCGAGCTGAATAGATTTAATTCTTTCTTTCCCATAGTA
AATGTGACTCTGGACCCAGAGACGGCCACCTCGCCTCGTCTCTCCAA
GGACCAGAAGAGCGTCCGATGGGAATACAGCCTGCAGGAATCCCCGACG
GCCCCGAGCGCTTCGACGCCGATCCCTGCGTGCTGGGTGTGAAACCTTC
ACCTCTGGGAGGCACTGCTGGGTGGTGGATCTCACAGAAGGGCAGTACTG
CGCCGTTGGGGTCAGCAGGGAGTCCCTGCCCAGGAAAGGAGCCGTCACTG
TTAACCTGATGAAGGCATCTGGGCTGTGCAGCAATGGGGGTTCAAGAAC
AGAGCCCTCACCTCCCCCTCCGACCCCACTGAACCTTCCACGGGTTCCCAA
AAAGATCCGCATCTCTCTGGACTACGAATGGGGCGAGGTGGCGTTTTTG
ATGTGGAGAACCAAATGCCATCTTCACTTTTCTCTGACCTCCTTTGGT
GGGGAGCGGCTCCGGCCGTGGTTCTGGGTGGAGCTGGGCTCCCTCTCACT
GCCAGATAACCCCGGAATCCCTGGAGGTGCTGTGGAGGTGCCTTACAGC
AGCTCTTCCAGACCGGGGTGGAATACTCTCAGGAAAAGCAGCATTAAAA
CCTCATTCTCCCTCTTCCAGTCAACCATTGTCATGCAAAAGAAAGGAAA
CCCATCCTCAATGTCATCAGCATCCTCCGTGTGTCATGTCTGGTGGCCCC
CATTGATGTATGGGGTGGCTCCTGTTGGTGTCTGGTGGCCCCCTATTGACG
TATGAGGTGGCCCCATTGACGTGAGGTGGCCCCCATTGACGTGAGGTGG
CCCCTATTGACATATGGGGTGGCTCCTGTTGATGTCTGGTGGCCCCCAT
GACATGAGGTGGTCCCCATGACCAGCCCTACCCTGGATCCAATGCCTCC
TGATTGCAGTTCCAACTCTAGGGACGTTAAACGACCCACAGAGAGGATG
GGGTCTCTTTGGTCTGATGGAGAGAGGTTGGCACCAGGGTAAGTCGCTG
CCTACATCACCCTGGTGTCTTGTCTCAGCAGCTGGTGTAAATTTCTGCC
ATCTGGGCTATTTCTGTAGAAAGCAAAGAAGCTCTGCTGGTGGGCAGCTC
ATCTCCCAGTGTGAAAAGCAAATGCAACGCATGCACCCTGCTATCCAT
GTGGCCATCCCTCTCCATCAGCTGTTGAAGGAGAAATCTGCACTCAGAAG
AGATTGAATTGGGCTCAGATCTGGCTTGGGAAGATGATGATTCCAACCAG
AGTCCAGGAGACTTTGGGAATGCATGAATCCTATAGGAAAATGGATAAC
CCTTCATCCAAGAGCAAGCTGGCATGATGCTCTGGGGTGAACCCATAA
TGCCACCTGGTTTTAAGGTTTGGGGTGGCTTACAATGTGCAGCTCTGCTT
CCGGCGAGGCACTGGGAGCCCTAAACCCATGGAGAGGTCAAACCACTGCT
GGAGGTCAATTGTGGGCCAGCTGCAATGGGAGGTAGGCAATTATGGACAT
CGCTGAAGCCACCCACGCTCTGGGGAACCTGGGTTTTACCTTTCACTG
CACTTTAATGGGATTTCTCATCAATGTCTGCATGTTCTTGGCCACCTGTT
TAAAAATATAATAATAATAATAATCTTTTGGCCCACTGCGGGATGAGC
AGCTGGTGGTTCAGCTCACATAAACCACACTTGAGACTCCCTGGAGA
ATTGCTTTCTTTTGGCAGCTGGTTCCATGTGGGGCTGTTACGCCCCCTCT
GCAGCTCATAGGCTTTTCTTACAGCCTCTGCTCCACCTATTGCTGAAAA
GGGGGAAATTTGAGATGGATCCCATTTTGTGAACATCTCCACCTGTGGG
TAATGCTCAGACCTCTCAGCCCTGTGGGTTTAAATTTCTCTTTCTGCAGCT
TAATGGGTTGGGATGTTCACTACTGCAATAATTAGTGATGGGATAGGGG
AGGCAGGAGAGGATCCAAGCAGGGGAAAGGGGAGGGGAAGGACATACTGT
GTGTGCTG

REPLACEMENT (REGLE 26)

FIGURE 10

SUITE 42

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COSMIDE.txt

AGAATACCATTCTCCCTATGCCAAAGCAGAACTGAGGGCAAAAATAGTG
GTTATTTTAAAAATATATATGTTTTTAATTGACTATCAACAGGGCGAATGGC
ACAAAGGTTGCATCACGCTGTGTGGTGGGTTTTGATGCAACTCAAAATTG
CAACTAGGAGTTCTGTGCTAAGTGCTAAGGAAAAATGAGATGAAAAATG
AGATGAGAAGCCGCCCAGCTGTTTAATTAAAGCAGTTTGGTGACTGTCGT
GCTATGGTGACTGAAGTAAGCAAGCACTGTGCTGCAAAATGCCCCATCTC
TCCTGGAAGTCGAGGATATTTCCCTGTGGCCAATAATGACAGAGCATT
TTAAGCCCAATCTTTATCCAGCCAAATCCACAATGGAGACACCGATCT
GCAGGGAGATTCCAGATAGCACATTCTGTGTTTCTTAAATAGGGCTGAT
ATTTCCCTCTGTCCCACATGTGATCCATCTGAGCTCACACAGCCCTTAA
AATCTGCAAGGATCTTGTTCTGCTGCCTGGCGGTGAGTGTCTTTTGGGG
CTATTTGGCACCATTTTGGCAACGGGAGTTGGCAACGTCAACCTGAGTTC
TTCCAGAGTTCTATGAAAAGCTTTAAATCGGGTTTTTGCATTTTTCCA
CGATCCACCTCTAGGGACCAAGCTGGTATTGGGGGGGGGGGGGGTGTGC
TTTCAGGGGGGTTTGGGTTCTGTTTGGGGGATATTTGGCATATAAAGGT
GGTTTTCACCTTTGGGATGGGCCTTGGAAGGAGTGTTTTGTTGGCTGTC
CCGTTGCCCTTCTTCTACAAAGCCTTCTTCTACAGAGGCTGCACCAA
GGTCTCTTTTAGCAGATCACAAAGAGAGGGCGCAAAGAACGAGTTAGAA
TTCAAGTTTTTAGGGTTGAAATATGGGTAGGATGATTGAGTCCTTCTCCT
TTGTCCGTACCAAGCCTGGAGATACCAATCTGAGATGTCAAACCTGCACAA
TGGAGCCTTCAGTGGGATGAACTTCAGGCCAGATGCCCAAGAGAGGTGTT
AAGTTTTGGTTAAAGCCACATCAGTAGCAATAGAAAGAAATGGGTGATT
CATCCCTTCCAAAACCTCAACTTTTGAAGAAATTAGGGAAGAAATCCCGC
TTCCGTGCTGAACCTTCTGTATTTTCAACCCAGGGCAAAGAAGGAGGAT
CGCGAGAGATTGGAGACCACAGCACCATGGCCTCTGCTGCTTCCAGAGCA
AAGGAAAAGGGAGAGGGGGCTCCCACCACCTATCCCAGAGCATCAGAT
GGGCAATGGATGCAGCAGCTCCGTGGGTGCTGGAGGTGGCACGTGGCAGG
AGCGAGGACGGCTCGGAGATACCGAGGTCATCAGCCACCGAAACCATCTC
AGGAAAGGGAATTTCCACACAAAACCTCCATTGGAGCACCTGGCAGAGAA
GCTGAAGCTTTTGGGGCTGGATGGAGACAGAGGGGAGAAGGAGAACTCT
GCTCGTGCGCAAGAGGACATTCCCCTCCAATGGACCACGGGATGATGGA
GGTCCCACTGGAGCCCCCATAAAGGAGTCAGTGCAGGAGGATGTGGTCA
CCCTGTGTTATTCCCTAAAGCCCTGTTTAATCCTTCATGTCCATGCTGAA
AACTTCTTCTCTGCGAAGTCCAACACATTGCATCTCTTCCCTTCTTCTC
CCATCACAATATCTCCCCAAACCCCTTTTCTTCTCCTCAGGAGCAGATT
CACAGCGATCTGGAGAACCTCAAGAAACAAAAGGAGGAGCTCTTAGAACT
CAAAAGGAGTGGGGAGAGGCGATGCCAAGACCTTCTGGTAAGAAGCTGTT
GCCTTCAAGCTGGAAAAACAGAGGTCTTTTGGGGTCCACGTTGTTGATT
TTCCACAACCTACAGACACGGACGGAGGCTGAGAGGCAGAAAATTGTGTC
AGAATTCCGTGAGCTCCGCCGTTTTCTGAAGGAGAAGGAGATGGTGCTCG
TGGCACGGCTGGGGGAGCTGGACAGGGCTGTGCTGAGGAGGCAGGAGGAG
GAGGAGGCCAAGGTGGAGGGGGACATTTCTCTCCTCGGCATCCTCATCTG
TGAGATGGAGGAGAACTCAAGCAACCCACACGTGGATTCTTACAGGTTG
GATTCTTACGGGTTGGATTCTTATGGGTTGGATACTCCATTGGACCCTCT
CCCTTCTTGTCCACCTTCTCCAAAGCTGGGGGAGATTGAACCATTTTTTC
CTATCTCTTTCAATTCCAGGATGCCAGAAGCAGCTGAGCAGGTATGTGC
TCCTTCAACCTCATTCAACGGGGTGGAAAGGGTTCCCATCCCCACACCC
ACGGATTCTAGCAGAGAAATGAGAAATGCATGTGATTGAGGCAAGGTTGG
AAGTCCCATGGGGTCAAAAAGTGCCTCAGTGTAGGAATGGCCAAAGAGA
AAGACCTCGTGGCCATTGGGGCGACCCAAAGGACCGCATTCTGTACGGAG
CAGGTTGGCATCCCCAAACCTGTGACAAAGGGACATTCTGGAGCCAACCA
CCTCAACCTCCATCCCCACATCACCAGAGATCCCCACACTCATCACCACC
AGTCCCAGCACTGATGAGATTGTGTCCAGGTGGGAGAGGGGCAGAACAC
GAAGGATGACAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TCCAGCAACATAAAATCCTCAGGGAGACGTTGGGGAGATTCCAAGGTAT

FIGURE 10

SUIITE 43

TGTGGACCACAGTATTCTTACCACATAGGATTTGCTTTGTACTGAAGGTT
GGGGGGTTTTTTTGGTCGTTTGAATAGGAGTTGTATACACTATTGGAAAAC
AATTTCATTAACTCACACTATCAATCATTCTTAGGCCTAAGAGCATCTG
TTTTTTTAGGACCAAATCCACAGATCCACATAAAATCCTGCACAGATAT
CCATGATAAACATGGTGGGAACGAAGCAGGCAGATGTGGGACATGACAT
CCAACCTTCTGTTTCATCCCCAGATCTTTTTCTATCTGAGCTGGAGAAGGA
GGAGGGAGCATCTGTAGGAGAAGAGGGAAAAGGTGAGTCCTTAAAGCATT
TTCTTTTGTCTCCATTGGTCATTTTTTTAGCCAAAATACTCGCTCAGAGC
ATCTGGAAAATGATGGTTTTTGAGCTCATTCTGGTTTTCTAAAGGTGATA
TAAAGAAGCTTTCTTATATTTTTCAGCAAAGGTTTTCTGAGCTGGAAAATAT
GGAGACATCGCTGATCCCAAAGTAGATTTGGGGTGCTGTTCCAGCTTTAG
GGTGATGCTCACCCATTTCTTCTCCATCCCCAACAGCGTTTGTACCCTG
GACCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CACTTTTGGGATGTGGAGGTGATGGGTGGTGCCACGTGGGCACTCGGGGT
GGCAGCAGCTCTGTGCCCAGGAAGGGTTGGCTCACTTTCCACCCCGATT
ATGGGATTTGGCTATGGGATGCTGTAGGAACAGCTTCCGAGCTTTCACA
TCTCCCCATCC

SUITE 44

WO 99/27132

PCT/FR98/02501

82/110
D12FOR.txt

GGGGGGCGATATGGGTGGTGGGACATGAGGGGGCCGGGGGGGGTTCGGGTC
TCACCCGCCAGCAGCAGCCGCAGCCCCGCAGCCATTGCTCTCCGCTGCTT
TCGCTTTCGGCTCCGCTGTGGCCCCACCCCTCCGTCACTTCGTCAATAT
TAATTTTAAATCCCTGAAACCCATTAAAAAAGGGTCGGAGAGGGAAAAC
TCATTTCAGGAACAGTGTTGGAAGAGGGGACATGGGTGGGACAACCCGGCT
TTCCCCACAGGCCGACCTAAACACAGCCACTGCCACCCACCCCGGATCCA
TGGGTGACGTAAGGATGAGGTTCCAGCACATATTGGACCCTTCTGCGTTT
GCATGG

FIGURE 10

SUITE 45

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E1REV.txt

GTGGGGGGCAGCGTCCGCGCTGACCTCGTCTCGCTGTGTTTCAGGGCGCC
CCGTGCGCGCGCTCCAGGTAACGTCCCGTCCCATTCCCGTCCCGTTC
CCGTTCCCGTTCGCGCTGCGCGGAGCGGCCCCGATCCCGGCGCGGGCT
CAGCTCTGCCCCGTCTCCCGCAGGGATGCTGAATTAGCTGCTGCCCCGCC
GAGCCGCTGCACCCGCACCCCCCGCTCTCCCGGCCGTGCGCTCGGCTCTC
CCTCGGGCTGCCACCGCGTCCGTTGGAGATGTCGCCACGATGCACGCTTC
GTCCCCATCCTAATAAACGCGCTGACTTTGACCCGCTGTTGCTGCCCCG
TGAATCATTGGGGACTTTCGTCGCGTGGGAGGAGGGGAGGGAAGTGAAA
GCTTCGTGGAGAAGTAAACCCAGCACCCCTATGGGTCCACGCGGACGTGGA
TTGGTGGGGATGGGGTGGGATTGGACTCTTGGTGGTCATTTCCACCCATA
GGGAGCTCGCGGCCACCCAGTGGTCCTCATATAGACTCCATGGTCACACC
ACTGTACCTTTTGGTCACCCCATGATCCCTGTGTTACCCTCCGGGGTCC
CTCAGTGGTTACCCACGTTCCCCCAGAGGCTCCTCCTGTGCGCTTCATC
ATCTACCCCATTTGACCACATACCCCCCTCCCCCTATGGATAACCCAAAG
CCATCACCAGTGGTGTGGGATGCAAACACGGGGCCCCGGACCTGTCCCT
ACAAGCACAGGGTGGTGACACAGCCCAGACAGTGTGCTGTGTCATTTGT
CACCAGGCAGAGGACACACAGCCACAGCCTGGCTCAACTCGAATAATATT
TTCTTTATTTACATGTTAAAGAATCGAAAGGTGGAAACATACAGTAAGA
TGAAACACGGCTCTAAGGGTCTAACAGTGGGGCAGGAGGGTGGGGGGGA
GGAAAAAAGAAAAAGGGAAAGAAAAACCAAAACAAGTAGAAAAA
ATGATACAGTCAACGTAAAAAGGGGTGGCCCTCCCTCCCCCAGTGGGAA
CATGCGGCGCTGCGTGCCGGGGGGTTTTATGTACAGGGGCGGGCAGCTC
CAATAAATTAACCTCCAATAACAATGAGGGGGGAAGGGGGGGTGCAGA
GCCCCCTCGTGGGTGGTTTCTTCTTTAAATGCTTTTTTTTTTTTTTGT
AATTTTTTTTAAATTTTTTTTTTTTAAATTTTTCTTAAAAACCCAAACCTT
TTTCTCCCCCCCCCTTTTTTTTTTTTTTTGGAAAAATCCCACGAGTCAG
GAGGAAAAAAGAAAAAGCCAACCTAACACAACAAACAGTAAACCT
GCTGGGGGGCACCGCGACCCCCCTTGTCCGACCCACAGCCCCACACT
GCCCTGGGGACGCTCGGGGGCTCCGGTCACACCGGGACCCCCAGCTGAG
TCCATGGGGCGTCCCTGGGCTGCTGGGGGGCTCTCGGTCTGCTCCATGC
CGGCCCGGTCTGTCAGAGCCGCTCGGGATGCTGCCCCATGTGGTGTGTG
GGGTTTAAACCGAATCCGAGTGTGCTGGTGTGCGAGGACGAGGAGCTGGAA
CTGGAGCTGCTGGAGTCGGAGCTGGAGCTGGAGGCGCTGAGCCGTGAAAC
AGCCACCTGCTGTGCTGACTCGGGCTTCTCGTTGGCTGCAATGGGACAAC
ACTGCGCTCAGCATCACACAGATCACACCCCAATCCCCTCCAGACCCC
ACACTACCCCTTTTTTGGGGGTTTCTTGGCTGAGTTGAGCTGCCCGCTGA
CGTCTGCAGCCGCTTCTCCAGCTCCCGCTTCTTCTCCAGCGCCAGTTCT
TCTTTCGTCTTCCCCACCGGCTTCTTCATGGCTGTGAAATTCAGGTTTCAG
CCCCACACCATCCCACCTCCACCCACGGGCGCCCCCTGAACGCAGCCCC
CCACTCACTCTCGCTATAGGGTTTGCGGGGTTTCTTCCGACGGCAGGACA
GCACGTAGCGCTCCAGCTCACGCAGTGTGGAGGGTTTGAGGGTCTCGAAG
TCGATCTCGATCTCCTCGGGGTTGGAATCACGCAGTGAAGGCTCCCGGGA
CTGGATGATGTGCACACACGGCCCCAGCTTCTCCCGGGCAGTTTGTGA
TGTCCAGGCTCAACTGCCTCTTCTCATCGTACGTATCGGTTTGTCTCTC
TCTTCTCTTCCGAATCGTAGAGCGTGGGCGGAGGCGGCAGCGCGCTTT
TGCTGCTTTCTTTGAGTTCTGTCAGGAAGCAAAGCACCATCAGGAAATG
AACCTCAGGAATCACCCACAGCTGACCATCATCCCCAAAAAACAGCCT
AGACTCACTTGGAGCTGCCCCACCGCTCCCCCGCGGCCACCTTCTTG
GCTTTGCGGAGCTGTGCCTGACGCGCCCGGCTCTTTCATCTCCTCCTCG
CCCTTTGTGCTTCTCCGATTTCTTCTTTTTTCTTTTTTCTCCCGCTTCTTT
TGGGTTTGGAAACGGGGCCCTGTGAGAGGGCAGCCAGCTGCTCGTGCACG
GCCCGCAGCTGTGGGGGGAGACAGGGGGTGAAGCGGGCATGGGGAGCAGG
CACAGGCAGCAGACCGGGCCAGCTCCGGCCCTCACCTGCTCCTGCAGCT
CTGCCAGGCGGTTGGCACGTTCTTCTCCGAGTCAGAGCTCTCCTCGCTG
TCTGATGAGCT

FIGURE 10

SUITE 46

84/110
E1REV.txt

TTCATCTTCATCATCCTCATCGCTGGAGGATTCTCGGAGGAGGATTTGG
AGAGGGCTCCAAGCAGTGGGGCAGACACTGAGGGTGGGCTGGCGTCTGC
GGCTCATCAGGCATCTTGGCGTAGCTGAACTCAAAGACATCTGAGAGAG
AGGACACAGAGGGGTAAGCTGACTGGGCTGGGGGTTACGGGGCTGCTGGG
TGACCCACCCACCTGCAGCTTGCGGGCCATGGCCACCACATCGTGGTCG
GGAGGGTTGTATTTGTAGCAGTTGGAGAACATTAACCGGACATCAGCGGC
AAACTCCTGTGCGTCATGGTAGTCCCGGTTCTCCATCTTCCGCTGTGGGA
AGGGAAGGCGTGAGCAGACCTCAAAGCCACCCCCACAAAGCCCCCATGA
GGCTGTGCCAAGGCCACGGAGTCCCCAAGCGAACCTTGATGGTGCTGAG
GTCCATGGGGTGTGATGATCTCGTGGTAATCGTGCAGCCCCAGCGCCG
AGGCATCGACCGGCTGTAGAAGGGCCATGCGTAGGCAGCGTGCTTCTTG
GAGAGCAGCTCCTTCAGAATCCCATTGCAGTATTTGAGCTGCTCCGACAA
TTTGCCCTTTTTGGAGGTCTGATGCTGCTGGGAATCCGGCAAGTCCTTCT
TGGGGGGTTTTGATGGGGCGGCCGCTCTCACGCCGTGCGGGAATTTTGGCC
GCCTTGGCCTCCAGCAGCGTGGCTGACGGGGAGGATTACCGCTGGTGGC
TATGATGGCGGTGGTGGTAGGGGTGGTGGTGTCTGCTTCCGCTTCACAC
CCTTTTTCTACCAAAATACAGAAAGGTTGATGAATGGGAGGCCAGCAC
GCCACAGAGCCTCCTCCCGTGAGCGAAGAGCTCCCATCTCCACCTTGG
CCACGGGTGGGTGGGCGCAGGCGCAGTCAGCACAGCCGGGGCAGTGGAG
TGCAGCGACTTGAGGAGCGGAGCGGAGATGACGGACGGGTGGGGAATGTT
GACAATGGTGGTGGCGATGTGCGGGGCTTGGGGTGTACACAGCGGTGTGGG
ACACAGAGGAGACAGCTGGCACTTGCTGAGCCGCTGTGAGACCTGCCAGG
AGCGCTGCGGACAGGCAGAACCCCCATTAGCACCAAGGTACCTTCAGTGC
TCTACCTGAAAGCGCAACCCAAAGAACCCAGGTACCTGCTGCCCGCGAC
GCTCCCTTCTTGTGGCTGTTTTTGGCCACTGGGACCACGATCTCCTGCTC
TTCTGGTGGCATTGTTGGGCCACCTTCTGCAGGAAGATCTTCTCCAGGGTTT
GGGCCATCAGCACAAATGTCATCTGTGGGCTACAGGGACAACCGAAACGTC
ACAGGATGCAGAGATGGCATCAAAGGCCTCAAAGCATCCATGCTGCAGTC
CTCACCTTGTTATAGATATAGCAGTTTGTGAACATGGTGTGAAGTCCTG
CATGCACTCAGCTGCCCCCAGTAGTAGTTGTTCTCCAAGCGCCGTTTGA
TCGTCCCCATGTCCATGGGCTGCTTGATGATCTTGTGGTAATCCTGCATA
GGGGATGGACAGTCAGCGCGTGTGGTAACCACTGCACCCCTCCAG
CCCCAGAAGCAGTGGTTTTGGGGTTTTTAGGAGCTCAACATCCCCAAAGT
ATCAGGACGTTGACACGCACACAGATCCGCTCTCGCACCATGCATCAAAA
GCAGGGCAAAAGGTGCAAAGGGATGGAAAAACACCTCCGGGTCTGGTCC
CCGCCGAGAGTGCCACCGTGTCTGTGTAGGGGACCTTCAGGTGCTCT
TGTGGGTGCTTACGCTATAGGGACAGCCAAAACACTGCTGTCCACAGCA
TGAGGTGCAATGGGGGCCACTAATGCTAAAGTAAGAGCAAACCTATGTGG
AATTTACCTCTGGGCTTTAAATCCTTGGGCGCCACAGGTACACAGGGGGC
TGGCGTTAATATTGGGGTCACAAGATGTCTTCTACAAATTCATGGATGG
GAATCTGCAAAACGCATTACAGGCACAAGAGATTAGGTGAGGAAACATCC
GGGTTCCCTCTAGAGCAGCTGCGTCACCTCACCCATAACCGTGCGGTGGC
ACTGGGAGGGGACAGCAGCTCTGAGGACATCAGGTACCTACTGGGGGGG
CTTCAGAGCCTGTGGAGTTGGGATTATGCCCTAAGAGAGGGCGAGGCCA
GCACAGCCCAGGCACCTGCAGCTGCATCTCTGTGGTGGAGCCCATAGAGG
GGACAATGCTGTCCCTGTGGCACTCTCAGGCTGGGGACCACGGCTCGGGG
TGGCCCTCAGCACCCAGGGGACAAGTCTGGGGACACACAGCCATGCTGGG
GGACCCACAGGAGGGGACACGTTACCGGCAGACCCAGCTTGACGGCGTCCG
ACGGGCTGACGGAAAGGCCAAGCGAACTGGTGCTTCCACAGGGCTTTTCAT
CACCATTGTTGCAAGTACTGCAGCTGGTTGGTGACCCGGCCGGGCTTTT
TGGGGTTTCGAGACCTCTGGCGGAGGGGGGTTTCGCCTGGGGGGTCTGTAGG
GCCGGCACCGAGGCCATGGTGGGGCTCTCGAAGCCCTCGTAAAGCAGCGA
GGGTTTGGGATGCGTTTGGCCGGGGTGGATTCCGTGCGCCAAACCCATAA
GCCCGGCATTTCCCTCCCCAGAATCCTGCAAGGGAGCAAAGACAACAT
CAGCAAGGATGGGGCCAGCGTTCCACCACCAAGGTGCACAAGAACAGCTC

FIGURE 10

SUIITE 47

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E1REV.txt

AAAAAAGGCCAAAAAAGTAATCAAAAAAGGAAGGTTGGAGCAAACAAA
GAGTCAGTGCAGGGGGTGACATCAGGGCCCAGCAGTTTCACCACCTCGGG
GTACGACAGCCTGCACTACAGCATGACAAGGCAGCACCCAAACACTGTGG
CCCTCAGCTGGATACACAACAGTGGGCTCCAAATGTCTGGGACGGGGGC
AGAATTATTTAAGTGGGGAATGAGGATTTAAGCAGCTGGGAGAGGTGG
GATGTCTGCAGCGTGAGGAGAATTTGTACCGGGAAAATACGGTGAATGT
CGAGCACTGGGGCTGCTTTCTCAGGCAGCTCCAGGGTGTTCCCATCCT
GCCAAGGACGTGGTGGGAATGACAAGGAAGGAAGGTGACAGAAGGACACA
GCGGCCCCAGTAGTGGCGGTACAGGGTGGGAGGACACGGTGAGACCCCTC
AGCATGGTGACAGTGTCCCCGAAAGCAGCTCAGTCAGCAGAGGTGGCAGC
AGGGCCCTAAGGGCCCTTGTGATGCTGACCCCAAGGACCAGGGGTATGAG
GAGTGGATAAATGGGGGTGGCCAGACAGGATCCATGGGAAAACAGGGCT
GCCAGGTTCCCTGTAGGATCTGTGTCCCTGCATCCCTGACAGAATTCACA
TGGACCACGGGGCTGCCGAGTCCCAACATCCCTGAAGGACCCACAGAAAT
GGGAAGTGGATAAATGGGAACAAGCAGCAGATCAATGGGACTCAGTGACC
CCAAACTCAGAGCTCTGTGACAGAAAAGCCCCATAACTCTGGTGGACATC
CACACTGCACCCTAATCCCTGGGCAATGAAGGGATAGCAGCAGGGAACCA
CTGTGTCCCTGTATCTCTGACCCCAAAGAATCCATGGAGATGGGGAATGG
ATAAATAGGGATGGCTCTGTAGAATCCGGGTCCCATTCCCCTCAAATAAT
CCATGGGAATGGCACTGTGGATGCATGGCCTTGAGTCCCTGTCCCTAA
AATCTGTAGGAATGACTCTGTGCTATGCACCTCCCGTGTCCCTGTAGG
ATCCATGGGGACAGCAGGCTGCCAGGTCCCCTGTATGATCCACAGCCCTA
AAAGCAGCTTGGTCAACAAATGGGAGGGAACAGCGGGTCCCTAAAGAGCG
CCAGGTGCGCATGTCCCTGTCCCCAAAGGACCCACAGGTACAAGGAACGA
ATAAACAGAGACAAGGAGCACTCAGTGGGATACAACCTGATGTCAGGTGCA
GAGCCTTTGAACACAGAAGCCCCATCTCCCCATAGGATTCAGGTCCCCAT
GCCCCTGTTGGAACCATGGGGACAGGGAGGCTGATGGATTCCCTGCAGGA
CTGAGTTCCTGTGTCCCTGACCCCGAAGAATCGATGGGGACAGAGAGTAG
ATAAACAGCGATAGCCCTATAAGATCCAGGTCCCGCGCTCCCTGTCAGGA
TCCGTGGGGACCGTGGGGCTGCCAGGTCCCCACGTCCCCGTCCCCAAGCA
ATCGATCCACGGGGATGAGGAACACATAAACGAGGACAACCGGCATACAA
ACGAGATCCAACCGGGCCCCGGGTGGAGCACCGGGACGCGGCAGCCCCATA
CCGCCGTCCCCGACGAACGCCATCCCCGGTTCATAACTGCCAACACCCC
ACAGCCCCCCCCCGGGCCCCCATTCCTGCCCTCATCACCTACTTGCTCTGG
GGATTACATTCTGCAGCATGCCGGCGGTGCGTGCCCGGCGCCTGGCTCC
CGGCTTCCTCCTCCACCTCCTCCTCCCGCGCGCCTCCTCCGACGTCC
CCCCCACTTTGCCACCGAGCAGCGCCGTTAAGGCAGCGGGCCCTCGGCC
GGGCATGAGGCGGGCGGTCCGGCGGGGCCCCGCGCGCGCCCTCACATCA
GCGGAGAAAATGGCGCGGGGCTGGATGGAGAGGGGGACCTTCCTGCT
CTCCGCTGCGCACAGAACC CGCGCGACGCCCGCATATAGAGCCGGGAA
AGCCGCTAGGAACCGGATAGATCCTCGGAAGGACGGTGTGAGCGGATGG
AAGGCGGACAGAGGGCGGATGGAGGCGGATGGTTCAGCGGGAGGGCTCCA
TCTTGGCTCGTAGGCCCCGAAGAGGAATCGGTGCCGGCGGGCGCAGGCAG
GGGTGCTACGGAGGCCGGGGAGGGTCCGGTGGAGCGTCCGGGAGCGCG
AAGCGGGGGCTGGGCCGCCCGGTGGAGGATGGAGGCGGATGGGGGCG
CCCCCAGCGCGCGCGAGCCCGACCCCGACCGTCCCTTCGTCCCCACGA
AATGGCGCGGCTCGGCCTGCCCGCGGCCCTTATATAGACACCACCTG
GGTGCTGATTGGTGGGTGGACGCGCTGACGTGAGCCACCCGCTTGACCC
GCCCTGCCGCTGCCTCATTGGACGGCGGTGCTCACC GCGCAGCGCTCCTC
TTGGCCGCCCGCACGCCACTCACCGCGCGCTCCCCCCCCGCCCTTCC
GCCCGGTACTGCGACGGTCATTGGTCGGTGCTGCCATTCGCGGCGCGCG
ATTGGCCACCAAGGATCACGTGAGGGCGGGCGCTGTTGGCTGTTGTTGTCG
CGCGCAAGGTGCAGAGGGAGGGGAGGGCTAAGGCGGGCGTCCGCATTT
TGTGTGGCGGGCGCAACGGGCGGGCGTCCCGGGGTTCCGACCCCTCC
GCCCAAAGGCTCCTCAGGGGGCTCAGCAGACCCCACTCAGTCCCTACGGG

FIGURE 10

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E1REV.txt

GCTCGTGAGGCTCTCCAGCCGACAGCGGCCATCGGGCAGCGGAGCCGCG
GCGGTCCGCGAGCCGCGGGCTGAGCTGTGGTGAGGTAGTGAGCTGGGTCC
CGGGGATCCTGAAGGCTCCTGAGGTAATCGCGGCCCTCAGCGCGGTCCCG
GGGCTTCAGTGCCACCCACGGTGGTACTGGGGCCCTCAGACCGTCCCC
TCCCCACTGCCACGGCGATCCGGAGGGGGGGGGTCCGAGGCCGCCCGT
GTCTATTCCGAGGTGCTCTGTGCTCTTCTTCCCCACGGCAATTCTGGAGG
GCTCACAGCTACTCCAGAGCAGCCCCATAACCGTCTGGGGGCCTACTA
CCACCCTACAGCAACTCAGAGCCTCCCCCACCACCAAAAAACAATC
CTGGAATCCCCAAGGCCATCCACACCAACGCTGAAGGTCTCAAAGCCCC
CCCTCCCCACACACACCGGTTCTAGGGTCTCAGAACCACCCACAGCA
ATCCTGGGACGTTCCACAGCCCCTCCGTAGTAATCTTTAGTTTCTCAAG
GCCAACCCGTAGCACGGGGGGCCTCCGCTGCCCTCCCCCTCGTGGCAATCCT
GGGGGGCTCAGTGCCACCTCACAGGAATTTCCGGTCCGCTCAGAACCTCTG
CAAAGCAATCCTGGGGTCTCGAGGCCACCCACACCGATCTCAGGGTGC
TCAATGCCACCCACAGCTGCCCCGGGGCCGTACAATCACCCACACC
AATCCTGAGAACTCAGTGCCACCCACAGCCAATCCCGGGGTGCCCCAT
TGCCCTCTCTAAAGCCTCCACCCCAATCCGGGGGTGTTCAATGCCACCCCA
CAACCCCCCTCAAAGCACTCCTGGATAACCCACGGACACCCCAACGCCCT
AAAACAAATCCCAGGGCGCTCAATGGAACCTCCCGCGCAACCTCGGGCTG
CCCCACGCCCCCTCAACTCAAGCAGACCCAGAGACCCCCCTTTTCTCC
CAACCCCTCCGGCCCCACACGCCAAAGGCTCTCAAAGACCCCCCCCCAGC
GATCCCGGACCCGAAACAGGGCTTTGGGGTCCCCCCCCACGGCGCTCCCGGT
GCCGCCCCCCCCCGCCCCGTGACACAGCACTTTGGATCCCCGCGGGCCCT
CCCCGCGCGCCGCCCGCGCGAACACCCAAACATGGCGCTTTTCGCCCCA
AAAGCGCCGGGCACAAAGCGGCGCCGCCCATTTGGTCTGTGCCCCGGCTC
CTCGCTTCCCATTTGGCCCCCTTCGACGGCGGAGGGGCGGAACCAGATTTGA
TGGACAGCTCATGCTCACGTGTCTCCCCCCCCCGATTGGGTCTTTTT
GGTTAAAAAATAAAATAAAATCATAAAAAAGGGCGAAGTTGCCCCATC
GTCACTCACCTGAGCCGCTCCACGCAGGGCCACGACCCCAACCCGATA
TCATCCTCGCGTCGCCCCCTTAAAGCCCCGTTTTTGGGGCAAAAAATCAA
AAAAACATCCCAGGGCAGAAAAAGGAGCCACGCGCTACGTGAGCTGCAC
CGTGATTGGCCACCCGCCGTACGTGACGGCCCCGCGCCACTCCGACGGC
CCCATTTCATGGAGCCCGGGCGGCTCCGCGGGGTCTATCGCCGCTCCGGA
GGGGGTGATGGCGCGCATGCGCAGTGACGGGGGCATGTGGTGGGGGGAGG
GAGGGGTGGGGCTGTGGGGATGCCCGGTGTTGCTGGGGGGCTGCTGTAGG
GTTGTCATGGCATTGCGAGGATGCAGCCATGAAGATTCACGGCATTGTAAG
TGTGCATCTGTAGGGGCCCTGGCATTGCAAGTGTGACCTATGGGAGTG
CCCGGCATTGCAAGGGTGCACCTCTGGACGCGTGTGTCATTGCAAGGGT
GCAGCTGTGGTGGTGAATGGCATTGCAAGGGTGTATCTATGGGAGTGTAC
AGCATTGCAAGGGCGCACCTATGGGTGTGCTTGGCATTGCATGCATGCAC
GTGTGGGGATGTATGGCACTGGGGGGGTGCACAGTGGGGGTGCTTGGGA
TTGCAAGGGTGAAGCCTATAGCAGTGCCTGGCATTGCAGGGTTCACGCGAG
GGATGCGTACGGCATTGCAGGGGTGCAGCTGCCGGCATTGCAGAGGGCCG
AACCCGCCCGTACGGTTGTGCAGCGCTTCCAGCTCGGAGGGCGCATTGCA
GTGCGGTGCATTGCAGTGCAGGAGCCACTGCTGCAGGGTGTACAGTGCA
CGCCCCGAGGATGTCCCCCTCGGCTCCAAACCCCAAAACCCACGCTTATT
ACCCCCCAAAACATACTTTTACACACAAGACACATTTTACCATCAAAC
CTCACGCTTTTCCCCAAAATCCCTCACAAAAACAAAATCCGCGCCGTGA
TGAGACACCCAGAGATCTACGGAGCCTACTCGTCCCCTGCTTCATTAAT
TAGAGCTGCTTATTAATTGCTTGGGGTGGCTCAGCGCCTATTACAGCGT
CGGGGCTCCCCGCTAGTTTCTTCTATCTAGTAACAAGTGACGCAAGGTAA
CTGCGGAGCGCGGCCATTGGTTGAGCCGCACGATCATCTCCTGTACAGC
GCTGGTGTTCGCCGCAGATCTGTTCTGCCTAGCAACCGATGACGCGTAAA
GCCGCGAGGCACGGCCATTGGCTAAACTGGTTGCCGGTAGCAGAGGGATG
GGGGCTGCGAGCGGGCGCGGGCGCTCGTGGCAGCGCTCTCGGGGCGGC

FIGURE 10

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E1REV.txt

CCTGGGGAGCGTCAGAGCCGGTAGGGGACGAGGGCGGGGGCGGTATGGG
TGGGCACGGGGTAGTGCCAGGGGTGTCCAAGATGTGTGCATGGGGAGTGC
AAGGGGCTGTGCAAGGAGTGAATGATGCACTGGGGCAAGGGGTGGGCATG
CACTGGGGCAAGAAGTTGTGCAAGGGGTGTTTGTGCATTGATGCAAGGGG
AGGATGAGCAGGACTGTGTTTGCATGCATGCAGGGGGTTGTGCATGGTGT
GATTAGTGCATTAGTGCAGCGGGTTGAGTGTGAGATGTGGAGTGTGTGC
AGTTGTGAAAGGGTTGCCATGCACGAGCTGATGTGCGCTCAGTGAGCGTG
CACGCAGCCTGCAGAGTGGGTACACCTGCAACGAGCATGCATGCAGCAGA
TGTGTCCATGCACAGTGTGTGTGTGCTGGTGTGTCCCATGTCCAC
GCCCTGTCTGTGCTGCAGAGCCATCGCTGCACACTCTGTCTGAGGTGCT
CTTCTGCCAGCCGGACACGCCGTGCTGGGGCTGTGAGTGGCCTTCGACT
CAGAGCAGCTCTTCTCATTGATGTCCCAACTCGCAGTGGCTGCCGCAG
CTCCCCGATGGCCCCCTCGTGGCCCCGAGACATCGAGCAGCCCCACGAGCT
GCTGCACGACGCCCGCTGTGCCGTGAGCTGCTCGATTGCTCACCAGAA
TCGCCACCGGGCCAAACCAATGCCCTGAAGCCAAGGGTGGGTGCTGCTGT
CCCCGCTATGACCCCACTGATGGGTCCCCAGCCGTGTGTTCCCAGTGATG
CTGACCCCAATGGACATCCCCAGTTGATGCATCCCCATTGATGCATCCCC
CACAGACATCCCCATTGATGCTGTCCCCATTGATGTGTTCTCAGTGGATA
TCCCAATTGATCCTGTTCCCAATGATGCTGTCCCAATGGACATCCCCA
TTGATGCTGTCTTGTGTAAGTTGTCTCGATTGATGCATTCCCATTGATG
TGTTCCCAATGGACATCCCCAGCTGATGCTGTTCCCACTGATCCTGTCCC
CATTGATGCATCCCCAATTGGTTTATTCCCCATTGATTTATTCCCCATGG
ATGTCCCCACTGATGCTATCCCCAGTAATGCTGTCCCCACTGATGCTGTC
CCCAATGATCCTGTCCCCAGTGATGTGTGTTCTTAATGGACATCCCCA
GATGCTATCCCCAACGATGTGTCTCACTGATGTGTCCCCAGTCCATGTG
GTTCCCAGTGATGTGTCCCCAACATATGACCTCACTGATGTCTCCCCAG
TTGATGCAATCCCCAATGATGCATCCCCAACATGCATTCCCCAATGATAT
TTCTCAATATGATGCTGTCCCCAATGATGCATTCCCCATTAAACGCACTC
CCACCGACGCATTCCCACCGATGTGTCCCCACTGATGCGTCCCCACTGAT
GTGTCCCCACTGATGTCCCCCCCCACAGGCATCCCGGTGGCCGACGTCTT
CCTGCAGCAGCCTCTCGAGCTCGGCTACCCCAACACTCTGATCTGTATGG
TGGGCAACATCTTCCCCAGCCATCACTATCAGCTGGCAGCGGGATGGC
ATCCCCGTACCGATGGCGTCACCCACCTCACCTACACCCCCACCGAGGA
CCTGGGCTTCATGCGCTTCTCCTACCTGGCGGTGACACCGCACTCTGGTG
ACATCTATGCTGCATTGTACCCCGGAGAGGGACAACATCTCTGTGGTG
GCTTACTGGGGTGAGTGGGGATGTGGGGGTGCTGCTTTGTGTCCCCGCAG
CGGTGGCTGATGGGGGCGGGTGGTGGGAGCAATGCTTTGTGTCCCTGCAG
TGCCACAGGACCCCATCCCTTCGGACGTGTTGGCCACGGCGGTGTGCGGC
GCAGTGACGGCGCTGGGCATCCTGCTGGCACTGCTGGGTTTGGGGCTGCT
GCTGTCCGCCCGCGCGCAGTATGTGGGGACAATGGAGACAGCAGGGAC
ACCCGCCCCGTACTCACTGATGTCCCCCATAAGTTGATCCCTCGGTGTGG
GAACGGTGATGGTGATGTAATTAAGCCCTTCATTTGCAGCGCGGTGTCC
TTGTTTGTCCCCACTCCGGGAAGGGTGGCAATTAATGGGGTTGGGCATTG
TCCCCATGGCCCCAGGTGGCAAAGTCTGATCCCATTCACCGCCCATGGG
GTGACGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGTGGCACGGAGGGGATGAAGGCAGCAGTGCTCCTGATGGGGCCAAGGG
GTTTCAGGGTGCTGGGGGCGATGGGGCTGGTGTGAGCTGCGGGACAGCA
GGTAGGATGTGGGGAAGTGTGGGGTTTTTGGGGTGAAGCATGGGGGTTTT
AGGGTGCAACATGGGGTTTTCTGGGGTGCAACATGTGGGTTTTGGGGTGCA
GCATGGGGGTTTTAGGGATGCACTGTGAGTTTTTGGGTGCAAAATGGAG
TTTTTGGGGTGCAACGTGGGTTTTGGGGTGCACTATAAGTTTTTGGGTG
CAACATGGGGTTTTATGGTACAGCGGGGCTTGGAGTGCAGCATGGGGT
GCTGCATGTATGCATAGTGCAACATGGGGTCTTGGTGTGCACTGTGA
GTTTTTAGGGTACAGAGTGTGGGTTTTAGGGTGTGGGCA
GTGCAGAATGAATTATTAGGGTACAACATGGGGTTTTAGGGTGTGGGCA

FIGURE 10

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GGGCTTTGGGGCACAGCCCCAGTGCTGTGCCCTCCCCATGCCCCAACGC
AGGCGCCTTCGTGGTGCACATGGCCAGCTCCTGCCCAGTCTGGCCAATG
GCTCCCTGGGCAGCTTCGACCTCACCATGGCCTTCAACAAGAACCTCTG
CTGTGCTACGACCCCGACGTCCACCGCTTCTACCCTTGCGATTGGGGGCT
GCTGCACACCGTTGCCACTTTGCTCGCCGCCATCCTAAATGATGATACCA
CATGGGTGCAGCGTGCAGAGGCACGCAGGCAGGCGTGCAGTGAAGTGGCT
GCACAGTTCTGGACACACACAGCACTGCGCAGGAGTGAGCACCCTGCAT
GCAAGTGGAGCATTGCAAACACGGGACGTTGCATGGGGGTGTTGCATGGG
GGTGTTCGAATGGGGTGATGCACAGCCGGTCATTGCATGAGACGCTGCAC
GGGGATGTTGCAAAGGGAAGTGCATGGGGACATCGCACAGCAGGTTGAAT
GGGATGTTGCATGGGGACTTTGCAAGGGAAGTTCGCACAGAGCATTGCAG
GGGATCCACGCAAGGAATTTGCATAGGGAATGCACAGAGATGTTGCCTGG
GAATGCTGCATGGGGTCATTGCATGAGGAAGTGCAGAGAGACATTGCACAA
GGAAATGCAAAGGGGCATCACTAGGGGACATGGCATGGGGCATTCTAGGG
AGCATTGCATGGGGACATTGCAAAGGGAATGCAAAGGGACATTGCATGGG
GACATTGCAAACAAATTGAGTGGGAGATTGCACCGGGATGTTGCATGGGG
ACATTGCATGGAATGTCCACCAACCACCTGCAGGGTGACACTGGGACC
ATCCCCAGCTCTGACCATCCCCCTTTGCTGCAGCACCACCCAGGTCCG
CATCGTCCCCATCCCCATCTCCAACGACCCCGACACCGTCCACCTCATCT
GCCATGTTTGGGGCTTCTACCCACCCGCGAGTGACCATCCAGTGGCTGCAC
AACGGCCTCGTGGTGGCCTCAGGTGACACCAAAGTCTGCCAACGGGGA
CTGGACCTACAGGACACAGGTGGCCCTGAGGGCCAGCACTGCAGCAGGGA
GCACCTACACATGCTCAGTGTGGCACTCCAGCCTGGAGCAGCCGCTGCAG
GAGGACTGGAGTGAGTTTGGGGATGGGGATGTGGCACCCACACCCACAG
TCCCCACGGCTCATTGTGCCACGCTGTCCCCACAGGTCCCAATTTGTC
CCCGCGATGATGGTGAAGGTGGCAGTGGCGGCCATGGCGCTGACGTTGG
GGTTGGTGGCACTCAGCGCCGGGGTTTTAGCTTCTGTGAGCGGCCACGG
GGTGAGGGATGGGGATGTGGTGTGGGGACATGTGTGACACCGAGGGTCT
GGTGTCCAGTGTGGGGGTGTACCTCCTCATTCATCATCTTCTGTGTGGCAG
CTCCTGGCTAGAGGACAGCTCCCGTCCGATGCGGGTTCTCACTCCAAT
CCTGGTCCCCAAATGATCCCGGTCCAAGTTCTGGTCCCCATCCAGTCC
TGGTCCCCATTCTGGTCTTGGTCCTGGTCTGGTTCTGCTCCTGGTCCCT
ATCCCTGACTCTGGTCCCGGTCCCCATCCGATGCCAGTCCAGTCCCTGG
TCCCCATCCTGGTCTGCTCCTTGGTTTGGGGACCTCAATGACTGGAAT
CCCATGTCCCAACATGGGGACCCACAGTTTGGGGTGAGGGGCTCTACCC
CCCAATAAAACCATCTGCAGCCCCAACCTCGCTCCAATTTCTGTTCCCA
CGTTGGGTGGGTGGGGCTCCAGTGTCTCCAGTGTCTCCAGCCGTCTATG
TCCCGTAAGCGTCGGCTCCACTGCATTCTGCTCCGAAACAGATGACGCT
ACCACGGCGCCCGCTCTGATTGGCTGCTCCGTGCCCTCTCTCCGTCCCAC
GTCCGTGAAGGGGGGGATGTGGGGTGAGGGAGCTGAGGGGGCCGCCCT
TCCCCCCCCCGCTCCCCCTCCGCGATGTTGGTGTATTGGGGCTGCTGC
TGGGAGCGCGGGGGCAGGTGGGGGTTTGGGGTTGGGGTGTGGGGGGT
CTCTGCCTAATGAACTCTGGGGGGGGGGACGTGGGGGTCTCTGCTTTA
TGGGACTGTGTGGGCGGGCTTGAAGGGGCTCTGCTTTACGGCGCTGGGTG
TGGGTTCTGGGAAGACTGTGCTCTATGGGATCATGGTAGGGGCTTGGGGG
GGCTCTGCTTAATGGCACTGTGTGGAGGGACATTGGGGGTCTCAGCCTTA
TAGGACCTTGGGGATGATTGTGGGGGTCTCAGCCTTTGCAATATTGAGG
ACACTCTGGGTGGTGGTGTGAGCCCTTAGGGCCCCCAGGGAGGGCTTAG
GGTGGGCTCAGCCTTTTGGGATACTGGGGTCTTTTGGGGGAGGGTCTC
AACTTTATGGGATGTTGCAAAGAGTTTGGAGGGGTCTCAGCTCTGAGGG
ATATTGGGGACAATTCGGGGGATCTCAGCCCTTTGGAACCTCAATGGAGGA
TTTTGGAGTGATGCTGAGGACTCAGCCTTTTGGGTTGCTGGGTATGATT
GGGGATGCTCAGCCTTATGGAATGGTGGGGACACTTTGTGGGGAGCTCAG
CTCTGTGGGATATTGGGGCACTTTGGGGGAGTCTCAACCTTTAGGACTC
CCAGGGAGGGG

FEUILLE DE REMPLACEMENT (REGIE B26)

FIGURE 10

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E1REV.txt

GATGTTATGTCCCATGGGGACCTCTGGGGGCTCCAAATGGGGATGAGGT
CGCTGCCAGCACTGCCATCTCCCCTCTGTCCCCCAATGCAGGTGCCTTC
ATGGTGCATGTGGCCAACTCCTGCTCACTGGCAGCCAATGGCTCTCTGCG
GGGCTTCGACCTCACCGTGGCCTTCAACAAGAACCCTCTGGTGTGCTACG
ACCCCGATGGCCACCTCTTCAACGCCTGCGACTGGGGGCTGCTGCACGGC
GTGGCTGGACAGATTGCCATTGCCCTCAACAATGACAGCACCTGGGTGCA
CGCTGCAGAGGCACGGAGACGGCGTGCAGCAAACTGGCTGCACAGTTCT
GGGCACAGACGGCGCTGCGCAGGAGTGAGCATTGCAAATGGGGCTTGTGC
ACGGGGCGTTGCGTGGGGATGATGTTGCATGGGGCATTGCATGGAGATGA
TGGTGCATGGGGTGTTCATGGGGACATTGCATGGGGCATTGCATGAAGA
TGGTGCATAGGGCGTGCATGGGGATGTTGCATGAAGATGTGTAGCA
ATGATGCATGGGGCATTCCATGGGGACGCTGCATGAGGGTGTGTTTAGC
AATGATGCATGGGGTGTGCTGCATGGGGATGTTGCATGGAGATATTGCATGG
GGCATTGCATGGGGTGTATCCATGCAGCGTTACATGGGGTTCTCAAGCAG
GGGATGTTGCATGGAAAAGATTGCATGGAAAATTGCACAGAGGTGTTGCA
AAGCATATTGCATGGGGATGTTGTATGGAAATTGGACGGTGGCTTTGAAG
AACATTCTGCATGGGGCATTGCTTAAGGGTCCCAAGCATGGGGATGCTGC
AAGGAAATGCTGCTGCTTGGTGGCCTTGCAGAGTGTGTTGCATGGAGTTT
GCTTCAAGGAGATGTTGCATGGCATATCATCTGCAGTTTTGCAGAGCACA
TTGCATTGCACATTGCACACTGCACAGAGCAGTGCAGTGGGCATCTCCCA
GCGTGTGGCACAACGCTGTTGCAAAGGACATCCACGAGGTGTTGCAGCA
AACAATGCGCAGAGCTTGCACAGAACGTGGGATATCCATGGGGATGTGG
CACAGAGCATTTGCGTGGGGAACTCTACAGGGAAGTGAGATGGGGAAGTTG
CACAGAGCGTTGCAAGGGGTATTGCACAGAGGGAACTTGCAGAGAATGGG
GCAGGAACCGTCCCCATCCCCTGCTGCTCACCATCCCTGTCCCCACTCCA
GCTCAGCCCCAGGTCCGCATCGTCCCCGCACAGACAGGGAACCCACGCGT
GCCCATCCGCTCACCTGCCACGTGTGGGGCTTCTACCCCCCGAGGTGA
CCATCATCTGGCTGCACAATGGGGACATCGTGGGACCTGGAGACCACTCA
CCCATTGTTTGCATCCCCAATGGGAACCTGGACCTACCAGACACAGGTGGC
CCTCTCGGTGGCCCCAGAGTGGGGACACCTACACGTGCTCGGTGCAGC
ATGCTAGCTTGAGAGGAGCCCTCTGGAGGACTGGCGTGAGTTGGGATCA
AGGGGGTGACACAGGGACAGCGGTGTCCCTGCTGTGTCACTGCTGGCTGT
GTCCCTGCAGGTCTTGGGCTGACGCTGGAGGTGACGCTGATGGTGGCTGT
GGCCACTGTAGTGATGGTGTGGGGCTCAGCTTGCTCTTCATTGGTGTCT
ACTGCTGGCGGGCCCAACCCCTGCCCCAGGTGGGTGCTTGAGAGGGACC
CTATGGGGCTCCATGGACCTCTAAGGGGTCTCTGTCTGGTTCCTATGGGT
CTCTGGGTTGCTGTGAATCTTCTTTCTCTGTGGTCCGTCTGGGGTAT
CTGTTGATCCCTATGGTGTGCTGTGGGGCTCTGTGGTCTCTATGGGTG
CTTCTGTTGGCCTCTGTGAGGTCTCTATTTGTCTCTATGCATCCCTTTGG
ATCTCTATGGGGTCTCTGCGGGTCATTACGTGTCTCTATGGGATGTGACC
ATTTTTGACAAGAACCCCACTCACCCCTCTATTCCCCAACAGGTTACG
CCCCGCTTCCCGGTCACAACTACCCCTCAGGTAACAGTGTCCCCAACTG
TCCCTGTCCCCATTGCCATCAATGAGGGCTGAGTGACCCCATCTCTCACC
CCATGTCCCTGCAGGCAGCATCTGATGGACACCTTCTGTACCAACTGTC
CCTGCGTGTCCCCATCCCTGACTCTGCGCGCTGGTGTGACATTAAGAC
ACTCTGCAGCCTCTGTTGGTGTCTCTGTGGGCTTTTGGGGTGGGTGGTG
TCACCGGGGAGAGGTTGGGTTGGGGTCATTGCATCCATGATGGTGATGGT
GATTGACATTGTGCACAGGGAGATGTCCAGGCGCCTGTGGGGTCTGTGTT
TTAGGGCCAGTTCTGCTCAGTGCCTCCGTAAGTGATCTGGATAGGTGCTC
AGTCATCCTAATTAAGGAGGGGACAACAGTGAATGGGGAGGAGCCGATGA
CTCAGGCTGGGAGTGGTGATCCCAGAGGTTTCCCTCTGCTGTCACTGACTC
CGTGCTTTCGCTTTTCGCTTCAACAACCTGAGGGAGCGCATTGCTGCCTGGCG
CCGATGACGTACATAAAACCCCGACTGCCATTGGCGGAGAGGCGCAGG
AGGAGCCAATGGGGGCGCGGGCGGGCGAGGAGTAGGAAAAGCTGAAG
GAGCTGCGCTGGGGTGGCGGCACTGAGAGTGCAGGGTGTGAGGCGATG

FIGURE 10

SUITE 52

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ElREV.txt

GGGCCGTGCGGGGCGCTGGGCCTGGGGCTGCTGCTCGCCGCCGTGTGCGG
GGCGGGCGGCCGTGAGTGCGGGCCGACCGGGACCCCTCCCCGCCGTAAC
CCCACCCCGGGGCTGTGCCCCTGGGATCCTCAGACCCCAACCGCGGCTC
ACGGCCTCGCTGCGCTCCGCCCCCGCAGAGCTCCATTCCCTGCGGTACGT
CCATACGGCGATGACGGATCCCGGCCCGGGCTGCCGTGGTTCTGTGGACG
TGGGGTACGTGGACGGGGAACCTCTTCGTGCACTACAACAGCACCGCGCGG
AGGTACGTGCCCCGACCGAGTGGATGGCGGCCAACACGGACAGCAGTA
CTGGGATGGACAGACGAGATCGGACAGGGCAATGAGCGGAGTGTGGAAG
TGAGCTTGAACACACTGCAGGAACGATACAACCAGACCGCGGTGAGCAC
GGCCGGGGCCGCGGCTCCGTGGGTGTGGGATGGGCTCCATGGCGCAGTGC
CGCCACACCCCGCAGGCCTGGCCCTGCGCGGGCGACCGTCCCGGGGCT
GCCCCTCACAGCCCCACCGCGCTCGGGGTGCCGCGTCCCGGGGGGACCCC
AACCCATCCCCGCTGCAGTGGGAGCCCCGGAGCCGGAGGGGGCCCTCACC
CCCTGCCCGGCTGTGTTTCAGGGTCTCACACGGTGCAGCTGATGTACGGC
TGTGACATCCTCGAGGATGGCACCATCCGGGGGTATCATCAGACAGCCTA
CGATGGGAGAGACTTCATTGCCTTCGACAAAGGCACGATGACGTTCACTG
CGGCAGTTCAGAGGCAGTTCACCAAGAGGAAATGGGAGGAAGGAGGT
GTTGCTGAGAGGTGGAAGAGTTACCTGGAGGAAACCTGCGTGGAGGGGCT
GCGGAGATATGTGGAATACGGGAAGGCTGAGCTGGGCAGGAGAGGTGAGC
GGGGTGGGGGTGGGGGGGGGGGGGGGGGGCGGACGCAAGTGTGGGGCTGGACGT
GGGGCGGGGGCTCATCGTGGGGAGCTCAGCCCCGGCCCTCACTGCCGCCCA
CCCACAGAGCGGCCTGAGGTGCGAGTGTGGGGGAAGGAGGCTGACGGGAT
CCTGACCTTGTCTGCGCGCTCACGGCTTCTACCCGCGGCCCATCGCCG
TCAGCTGGCTGAAGACGGCGCGGTGCGGGGCCAGGACGCCCACTCGGGG
GGCATCGTGCCCAACGGCGACGGCACCTACCACACCTGGGTCAACATCGA
TGCGCAGCCGGGGGACGGGGACAAGTACCAGTGCCGCGTGGAGCACGCCA
GCCTGCCCCAGCCCGCCTCTACTCGTGGGGTGAGTGAGGGGATGTGGGG
CTGGGGGGCTGCGGGCTGCCCCCTTCCCTGCTGATGGCCCCGCTCTCCCC
CAGAGCCGCCACAGCCCAACCTGGTGCCCATCGTGGCGGGGGTGGCCGTC
GCCATTGTGGCCATCGCCATCGTGGTTGGTGTGGATTTCATCATCTACAG
ACGCCACGCAGGTAAAGCAGAGGGGTGCAGGCGGGCAGTGGGGGCTGTA
GGGGGATCTGGGTCCCCCTTGGGAGCCCCCAACCTGGCTGTGATGTAAC
CTGTGATGAAGCATCTCTGTCTGTCAGGGAAGAAGGGGAAGGGCTACAA
CATCGCGCCCGGTGAGTGATGAGGGCAGCGCTGTCCCCACCTCTGCCCA
GTGCCAGGGTGGTCTGCGGTCCCTGCTTTCTCCAAGGTACCCATTCTCT
GGTGCTTGGGGCTGCTCCATGCCCCATAGGGAGCACAGGGCTGGATCTCA
CAGCTGTTCTCCCTTATAGACAGGGAAGGTGGATCCAGCAGCTCGAGCA
CAGGTGCGGTGTGGGGCTGTGGGTGGGAGGGGTCCGTGTGCTCTCTGTG
GTACTGCCCAGGGCTGGGCTATGCTGGGGCTCTGCGGGGAGACCCCGGA
GCAGAGGGTTGGGATGTGAACCTGGCCCCGTGGGACATCATCCCTTCTCA
TCCCCACAGGGAGCAACCCCGCCATCTGAGTGCTGTGCTTCAGCCTGCAA
GGAGCCAACAGTCCACACCAGCATTTGGGGTGGTGATGGACACAGCCCC
ATCCTCCTGACCTCTCACATCTCATTCTGCTTCTCTATGCTGACTGTTATG
CTTTGCTGCACTGCTTCTGTGAAATAAATGATGGGCCATTCTGTGCT
CAGCTTGCCCTGCATTCTGCACTGTGCTGTGGTTGGGGATGGGGTGGGTGA
GAGGACCGTGTCCAGTTTGGCTGCTCAGGGTGCAGATGTGGCCCTGTGC
TGAGTACCCACAGCCCTCCCCCCTATCTGCCTGCTGCTCACTCCCCCTT
CTGTACCCCATCCCTTCTCACCTCTCCTCTGTGACCCCATGCTGGTGGT
TGCTTGCTCCCTGTCTGGCAGAACTCTCATTTTCCCAATGGCATCCCTG
GGTGTGGGATGTGGTCTCCTTGGTCTCCCCCAGCAGTCACTGCACAT
ATCCACCCCACTTCCCCCAGGTTGTTGTCCACAGCACTCCTATTTCC
CTCTCCCCCCCCCCCCCCCCCCCCCGCCCATCCAGCTGCCTCTGCAATC
CTCACCCCTTGCCACACACAACCTTTGCGCACTCCACCTCCCTCATCCCGC
CCTTCCCCCAGCTCTCTGTCCCTGCTGGCCCCCTCCCCCCCCCATT
GTACCCTA

FIGURE 10
SUITE 53

E1.REV.txt

FEUILLE DE REMPLACEMENT (RÈGLE 26)

SUITE 54

92/110

E1REV.txt

GTCAATGTCCCCCTGTCCCAGTGTCCCACAGCTGTGCTATCTCTGTGCT
ATGTCCCCTCATGCCATCATGTTCCCAGTGTCTGGAGCCCCCATGCCGC
CCCATTCCCACGTCACTGCATCCTCTGCCCCAGAGCCCCCTGAACTGTTG
TGCTGTACATCCTGATGTCCCCATGCCATCAAATCTATGTCCCACAGT
CCCCATGCCATCATATCCCATGACCTGCCATCTCCACACCATTATGGCC
TCCAGCCCCGTTGGCATTCTGTCCCCATCTCCTGACATCTCAATTACATCA
CGTCTCCACATCTCCAGCCCTATCCCACCATGTCCCCATGCCCCCAGT
CCTATCCTATCATGTCCCCACATCCCCAGCCCCATCCCATCACGTCCCC
ATGCTATTGAGCCACCCCATCCCATAACCACTGGTCCAGAGAGAGGCAG
TGAGAGGGGCCACATCCTTCTTCTCCAGGCGGTGGCTCTGCTGCAGGCGC
TGCCCGTAGTGTGCAGCCGCCCCATCCTCATTGGCAAAGCTTCGCACAGT
GGCCATGGCCTGGAAGGTCTCCACTGCCACCTCGCTGGCCCGGGCCTGCG
CCTTCTGCATCTGTGGTGCCAGGGCCTGGGGACAGCAGTGTCTTGCAGG
GCGGGTGGGAAGGGAATGGGGCTGGGGAGGGGACAGTGCATGTATGGAG
GGAACAAAGAACACGTGGAGGGGATGGAGGGGACATAAAGGGGACGGTGG
GCATGTGGAGGTGACAGTGGGGGCATGCAGAGAACAGAACCCATGTGGAA
GGGATAATGGTCACACATAGGGAATAATGAGCACATGGCACGGATGGTGG
ACGCATGGAAGGGGCATGGGGCACGTGGAGGGACAGCGGTACACAGAGG
GGACAACAGCAGGAGGATGGTGGGTACATGGAGGGGACAGTGGGCACATG
GATAGGGCAATGAGTACATGGTGGTGACACTGGGCACATGGAGGGGACCA
GAGGCACATGGAGGGGACCAAAGGCACATGGAGGTGCAGACAGCAGCCCA
TACCTGCCGGAAGTGCCCCACAGCCCTGGGCAGTGCCAGCAGCAGTGGCA
GCGCCAGCGCGGTGAGCAGCGCCATGCGCGGGGACAGCCAGGCCATGGTG
GCGAAGAGGCGAGAGGCCACGTGCCAGATACCACAGCAGGAGGCTCAGCGC
CTCACCCAGCGCCTCGCGCACGTCTCCGCATCCCGCGTCACCCGCATGG
CCACATCCCCTGCCGGGTGACAGCGCCGTGAGTGCCACCCCTGTCCCTTA
TCCCCGTGTCCCCTCCCAGCCCGGTGCCCTCACCGGCCCCGTGCGCGCG
CAGCTCGGTGATGCTCTGCCGACGACGGCGGCGAAGACGCGGCGCTGGA
GGCGGCTCTGCGTGCGGCTCAGTGTCCCCACGAAGGTCACATCACACACC
AGCTCAGTGACAGCGCTGTGACGGCAGTGGGGTGTGAGGGGGTCCCAGCG
TGCCCCCTGCCCGCAGCGCTCCCCCTATGCCAGTACCTGCTGAGGCCC
AGCAGCACCATGGGACAGGATGGCTGCCAGCTCATCCTCGCGGGCCACCCA
GTCGCTGGCTCGCCCCATGTAGTAGGGCACGGCCATCTCGCCTGTACCA
CAGCAGGGTCAAGGCATGGGGACCCCCCGAGGAATGGTCCCCAGGAG
TTCTGTGCTGCACCCCCAGTTTGGTGTGACCCCCAAAGCTCAGAGGTG
AACCTCCGAAGCTCATTGTTGCCCTCCAGTTGGCTGCAGCCCCCACCCC
ACCGCAAACCCATCTTATTCCCATTCAATCACCGCCCCCACCCCAACCC
GACCCCAATTCTATCTCCATCCCCATCCCTACCCACCCCAACCCCATTT
CTATTCTATCCCATTCTACCCACCCCAATCCAACCCAGTCCCATCT
CCATCCACACTCCATCACATTCCCATTCCCACCTGTCTTCAATCCCCAT
TCCATCTCCATCCCAAACCTCAGCCCCAGTTCCCATTCTCTCCCCATCCC
CACCCCATCTACCCAGTCCCAATCCCAGTCCAAACCCACATCATTACC
ATTCCATCCCAACCCATTCCCAGTGCCAGCCTATACCCATCCTTACCC
CCACCCCAATCCCATCCCATTCCCATCCCATTCCACGGCTACTTCCAT
CCCCAATCCCATTCCATCCGGTTCCCAATCCCATCCCCATCCCTACCCCT
ATCCCCAGCCCCACCACAACCCCATCCTCATTCAAATCCCAACCCCACTC
CGATCCCCTCCCCTCCCCCGCCCCGTACCCAGCGCCGAAGCCGCCAT
CAGACCCATCACCAGCGCGCAGCGCGCGCTCCGGGCTCAGCGAGAGGA
GGAGGCGCGCAGCCGCGCCATCTTCCCCATCGCGGCCCCGATCCCCCTC
CGGCCCCGATCCCAATGCCCGGCAGCGCGCGGAGCTTCTCGGAAACGAGAG
CGTCTCTCATTGGCTGAGGCGGTGCAGCAGCGACGCTGCTCATTGGTCGA
GATGGTTTCGCGTCATCAGTTGCCAGGCAGATCGGAACACTGCAGTTTGG
AGAGGGGCGGGTGATTGAAAGTGAAAGTAACGGCGGAGCGGGAAGGAGAT
GGAGAGCGGCGCGGTGAGGGGCTGGAGGGGGCTGGAGGGGGATGGACTG
GTAGGGGCTGGTGGGTCTG

FIGURE 10

SUITE 55

FEUILLE DE REMPLACEMENT (REGLE 26)

93/110

ElREV.txt

GTGGGGACTGTGAGGGGCTGGAGGGATCTGATGGGGACTGGAGGGGTTT
GGTGATCGCTGTTGTGTGCTCCAGGCTGGGCTGTGGGGAGCCGGACTGGA
AGTGGGGGCCGTTCTAAAAGCACTGCTGTGTGTTCCAGGTGCTGAGGGGA
GCTGAGGACCTGCACCAGGAGCACCCCGGGGAGCCACCTGGTCCAGCTG
TGCACCAGAAGCTCTGGGGATCCCCACCCACAGCCATGGCGATGCCGCC
CTACATTCTGCGCCTGTCATGCACGCTGCTCCTGGCCGACCTGGCCCTCA
TGTGGCCCTGGCCCACTTCTTCCCAGCACTGGCCCACTTGGGGCTGGGTG
GGCTCCTGGCTGGAGGCCGGGCTGCGCCTCCTGGTGCTGGGGGGGGCCGG
GCAGCTGCTGGCCCCAGGGGACCCCGTGGGGCTGCAGTGCTGCTGAGCC
TGGGCTGCTGGCCCCAGGGGACCCCGTGGGGCTGCAGTGCTGCTGAGCC
GCTGCCCCGGTGCTGCTGGCCATGGCAACGCCGCTCCTGGCTGGTGCTGAC
CCACGGGACAGCTGTGGTGGCATTGCTCACCTGGAGCCTCCTGGTCCCCA
CTGTGGCCACTGGGGCAAAGGAGGCAGAGGCCTGGGTGCCCCCTGAGGCGG
CTGCTGGCCCTCGCCTGGCCGAGTGGCCCTTCTTGGCTGTGCCTTCTT
CTTCTCGCATTGGCTGCACTGGGTGAGACCTCAGTGCCCTACTGCACCG
GGAGGGCTCTGGATGTCTCCGCCAGGGGACGGCCTCGCCGCCCTTACC
GCTGCTGTGGCCTCATGTGCTGGCCTCTGCCAGCAGGTAGGGACCCCA
CATCCCTCCACAAAACCCCATCCACCTCTGGTGGTGGTGGTGGGTTTG
GGGTCTCTGTCCATATCTGGGGGTCTCTGATGGGTCTGGGCACTCCA
CTGACCCTTTGTGATTGTCTGAAGGGTTCTGGGCTCTCCATTGACCCCTG
ATGGGTTTTTGGAGTCGCCCCCAATTCCTTCCAGCTCGCTGTTTGGCG
GCTGCCGCGGTGGCCTCTTACCTTCATCAGGTTCCGCTTCATCTTGGCG
ACCCGCGACAGCTCTTCTCCAGCCTGGTGTACCGGGACCTCGCCTTCTT
CCAGAAGACCACAGCAGGTACAGACTGGGGGCACTTTTGTCCCTGTCCCC
ACACCATAACCCCAAGCTCACCTACTCAACTCCACAGCTGAGTTGGCCTC
CCGGCTGACCACCGATGTGACGCTGGCAACGCTGTTGGCACTCAATA
TCAACGTCTATGCTGAGGAACCTGGGGCAGGTGCTGGGGCTCTGCGCCTT
ATGCTGGGGCTGTCCCCGCGCCTGACAATGCTGGCACTGCTTGAAGTGCC
GCTCGCCGTACCCGCACGGAAGTCTATGACACCCGGCACCAGGTGATAG
CAGGGATGGGATGGTAGGGTTGGGGTGACAGGGATGGAGGCAATGGCAAT
GGGATGGGAACAGTGGGAGTGGGGATAGTGAGGTGGGGATTGTGGGGTCA
GGGTGGCAGGGATGAGGGCAGCTGCAATGGGATGGGAACAGTGGGAATGG
GGAGAGCAGGATGGGGATCATGGGTCCAACACAGCAAGGATGAGAGGATG
GAGAAGAGTGGAGCAGGAATGGAAGTGGGATGGCGAGTACTTGGCCATCC
CATGGGTGCTGACACCCACTGTCCCCCAGATGCTGCAGCGGGCCGTGC
TGGATGCAGCAGCCGACACCGGAGCGGCAGTGCAGGAGTCCATCTCTTCC
ATTGAGATGGTACGGGTCTTCAATGGCGAGGAGGAGGAGGAGCACCGCTA
CAGCCAGGTGCTGGACAGGACCTACGGCTGCGGGACCAGCGGGACACAG
AGAGGGCCATTTTTCTCCTCATCCAGCGGGTGAGGCTGACACGAGGGGAC
ACCCTGGTGCTGCTGGGTGGGATCGGGACATCCCCGCTGAGCCCCATCCCCA
CAGGTGCTGCAGTTGGCCGTGCAGGCACTGGTGCTGTACTGTGGGCACCA
GCAGCTCCACGAGGGGACCCCTCACTGCCGGCGGCCCTCGTTGCCTTCATCC
TCTACCACTAAAGCTGGCAGCTGCGTGACAGGTGAGGTGAGGCAGTGGC
TCCTCTGCCACGGATCCCCATGACTGTGGCCACATCCCCGTGTCCCCAC
CCTGGGTGCTGTGCCTGGGGGTACATCCCCATGTCCCTATCCTGGGTGC
TGTGCCATGCAGGCACTGGCGTACTCCTATGGTGACCTTCTGAGCAATGC
AGCGGCCCGCTGCAAGGTCTTTGATTACCTGAACTGGGAGCGAGCTGTGG
GTGCTGGTGGCACCTACGTGCCACACAGACTGCGAGGCCACGTACCTTC
CATCGGGTGTCTTCCCTATCCCACTCGCCCTGAGCGCCTCGTCTCTGCA
AGATGTACCTTCGAGCTGCGCCCCGGTGAGGTGACGGCGTTGGCGGGGC
TGAATGGCAGCGGGAAGAGCACCTGCGTGGCACTGCTGGAGAGATTCTAT
GAACCTGGTCCGGGGAAGTGCTGCTGGACGGGGTGCCGCTGCGGGACTA
CGAGCACCGCTACCTGCACCGCCAGGTGAGGGGGTGGGGGGAGATGTGGC
TGCACTGAGCAGTGCTGGGGCTGAGCCTCTGCCCTGGGGCAGGTGGCACT
GGTGGGGCAGGAACCCGTGCTCTTCTGGCTCCATTCGGGATAACATTG

FIGURE 10

SUITE 56

[illegible]

SUITE 57

95/110

E1REV.txt

TTATTTTACAGGAAGCAGTGCAGGCAAAGCATAACAGTCAGCATAGGAAG
CAGAATGAGATGTGAGAGGTCAAGAGGATGGGGCTGTGCCCATCACTGAC
CCCAAATGCTGGTGTGGACTGTTGGCTCCTTGCAGGCTGAAGCACAGCAC
TCAGATGGCGGGGTGCTCCCTGTGGGGATGAGAAGGGATGATGTCCAC
GGGGCCAGGTTTACATCCCAACCCTCTGCTCCGGGGGTCTCCCCGCAGAG
CCCCAGCATAGCCCAGCCCTGGGGCAGTACCACAGAGAGCACACGGACCCC
TCCCAACCCACAGCCCCACACCGCACCTGTGCTCGAGCTGCTGGATCCAC
CTTCCCTGTCTATAAGGGAGGAACAGCTGTGAGATCCAGCCCTGTGCTCC
CTATGGGGCGTGGAGCAGCCCCAAGCACCAGGAATGGGTACCCTGGGAGA
AAGTGCAGACCCCAGGACCGCCCTGGCACTGGGCAGAGGTGGGGGACAGC
GCTGCCCTCATCACTCACCGGGCGCGATGTTGTAGCCCTTCCCCTTCTTC
CCTGCAGACAGAGAGATGCTTCAGCACAGGTTTACATCACAGCCAGGCTG
AGGGCTCCCAAGGGGGACCCAGATCCCCCACTGCCCGCTGCACCCCTC
TGCTTTTACCTGCATGGCGTCTGTAGATGATGAATCCAACACCAACCATG
ATGGCAATGGCCACAATGGCGACGGCCACCCCCGCCACGATGGGGCACCAG
GTTGGGCTGTGGCGGCTCTGGGGGAGAGCGGGGCCATCAGCAGGGGAAGG
GGCAGCCCGCAGCCCCCAGCCCCACATCCCCTCACTCACCCACAGTA
GAGGCCGGGCTGGGGCAGGCTGGCGTGTCTCCACGGGCACTGGTACTTGT
CCCCGTCCCCCGGCTGCGCATCGATGGTGACCCAGGTGTGGTAGGTGCCG
TCGCCGTTGGGCACGATGCCCCCGAGTGGGCGTCTGGCCCCGCACCGC
GCCGTCTTCAGCCAGCTGACAACGATGGGCCGCGGGTAGAAGCCGTGAG
CGCGGCAGGACAAGGTCAGGATCCCGTCGGCCTCCTTCCCCCACTCGC
ACCTCGGGCCGCTCTGCGGGCGGGCGGCAGTGAGGGCCGGGCTGAGCTCC
CCACGCTGAGCCCCCGCCCCACGTCCAGCCCCACACTGCAGCCGCTCCCC
CCCCACCCCGCTCACCTCTCCTGCCAGCTCAGCCTTCCCGTATTCCAC
GTATCTCCGCAGCCACTCCACGCAGGTTTCTTCCAGGTAATTCTTCCACC
TCTCAGGTTCACTCTCTTCTCCCATTTCTTCTTGGTGGGAAGTGCCTCT
GGAAGTGCCCGAGTGAACGTATCGTGCCCTTGTGCAAGGCAGTGAAGTC
TCTCCCATCGTAGGCCATCTGATAATACCCCCGGATGGGGCCGCCCTCGA
GGATGTACAGCCGTACATCCACTGCACCGTGTGAGACCCTGAAACACAG
CCGGGCAGGGGGTGAGGGGGCCCTCCGGCTCCGGGGCTCCACTGCAGCG
GGGATGGGTTGGGGTCCCCCGGGACCGGGCACCCGAGCGCGGTGGGGC
TGTGACGGGCAGCCCCGGGACGGTGCCGCCGGGCAGGGCCAGGCCTGGGG
GGTGTGGGGCGCACTGCGCCATGGAGCCCATCCACACCCACGGAGCCGC
GGCCCCGGCCGTGCTCACCGCCGGTCTGGTTGTAGCGCCGCTGCAGTATG
CCCAGGTTCTCGCGTCAATCTGCTCATTGCCCTGTCCGATCTGCGTCTG
TCCATCCCAGTACTGCTGGTCCGCCTTGGCCGCTATCCACTCGGTGCGGG
GCACGTACCTCCGCGCGGTGCTGTTGTAGTGACGAAGAGTTCCCCGTCC
ACGTATCCCAAGTCACGAACCACGGCTGCCCGGGGGCGGGATCCGTAT
CGCCGTTTGGATGTACCGCAGGGTATGGAGCTCTGCGGGGACGGAGCACA
GCGGGGCCGTGAGCCGCGGGTGTGGGTCTGAGGATCCACGGACACAGCC
CCGGGGTGGGGTTACGGGCGGGGAGGGGTCCCGGTCCGGCCGCACTCACC
GGCCGCCGCCCCGCACACGGCGGGCAGCAGAGCCCCAGGCCAGCGCCC
CGCACGGCCCCATCGCTCGCACCGCTGCACTCTCAAGTCCGCCGCACCC
AGCGCAGCTCCTTCAGCTTTTCTTACTCCTCCGCCCCGCCCCGCGCCCC
ATTGGCTCCTCCGTGCGCTCTCCGCCAATGGTAGTTGGAGTTTATGTGA
CGTATCGGGCGCCAGGCAGAATGCGCTCCCTCAGGTTGTGAAGCGAAAG
CGAAAGCGCGGAGCGGGGGAGGGGATGGGCGCGGTGTGGGAACCCCCGGC
CCTTCGAGCACGGGGGGGCACCCGGGCTGTGTTTCGCACGGGGCCGCTCC
TTACCCCGGGGGAGGGGGCCGAGGGTCTCTGCCGGGAGGACGGGGGCCGT
GAGAAGAGGAGGAGTCACTCTCCATTCCAGTCAAGGAAGTGTGGGGGG
GGGGTCACATCCATAGGGTTAGAGGCTCCGTGTCCGGGGGGGAGGGGGTG
GTGACAGTGGTGTCCCCAGGGCTTCTTTGGGATCAGTGCCATTTCCCC
ACAGCGCCGCCCCACACCGCTTCCCCACATCCACGTGGTCCATCTGAGGT
CGATGCCCTCAGGGTCTGCAGGTGGACCCCAATGTCCACCCCCCAAGTTA

FIGURE 10

SUITE 58

ATGATTGACCCCAACCCCGCTGTCCCTGCGCCACTGCTCCCATCTGCCCC
ACACTGCCGGAGCCATGGGGCCTCACTGGGCCTTCAGCCTCTTCCTCCTC
CTCTTCCTCACTCCCTTAATGAGGGCCAGCTCCCAGGACCCTGAGTATGG
GGCTATGGGGTGTGTTGTGGGGTAGCTATGGGACTATGAATGTTCTGCAGT
GCCTATGAGGGACTATGGGGCACTGGTGGGGCTGGGGGCTGCTATAGGAT
TGGGGTGTGATGGAGTCTGGGGGGACTAAGGGAGATTTCTGTGTGGTTGG
GTGGGGTTATGGGGCCAGAGCTGGGGGGATTCTATGGACCTAAGGGGTG
TCTGGATGCTTATGGGATCTGGGAGGGCTTATGGAGCAGTTATGGGGCTG
GTGGCTCAAGCAGTGTTCCTCAGGTTGGTGCTGGTGGCCCCCGGCGCG
TGGCCTTGGGGACCCCATGGGGCTGTTGCTGGCAGCTGTGGGGCCGGTG
ACCGGGACGGTGACTGCATGGGCTGAGGGGGACCGTGGGGCTGGGCCCTG
CACCTCCCAGTCCCATTGCCCCTCACACCCCAACAACCTTCAACCAGC
TCCTACAAATTGAGGTATGGGGACACCGGGGGATATGGGGACACTGGGGG
ATGTCTCTGGGGTGGGGGGTGGGGGACACCCCTGTGGCACACAGGGAT
GTGTGCACCCCTGGGTCCCCTCCTGCCATGTCACCCATGTACCTCACAT
CTCCTTCCCCAGAGTTCCTCCCATGTCCCCATAACCCAAACACCTCCTGC
TGTGTTCCCATGTCCCTTATAGGTCAACCCAGTGCAGGCAGAGCGCTGTG
GGGCGCTGTGGGGTGGGGGTGCTCCTGGAGGCCACAGCTCCCATCTG
CCCCCCCCCAGTACCAGGAGTCTGAGTGTGGCCCTGGGGGGCGCGGGG
TCACCTCATTGTGCAGACAGACAAACCTCTCTACGCCCCCGACAGACTG
GTGAGTGTCTCCACGTCCACCCTAAAGCCATCCCTCATCTGCCACAGTTC
TCCCCCAGTGGCCCAAATGCTCCAATTCCCCTAAATCAACCCCAAAATT
CTCCCCAAAGCCCCCTCAAATCTACCATGAATTCCCCTAAATCCACCCATT
TTACCCCTACATTACCCATTTACCCCAAATTCACCCCCAGCACACCCCA
AATACCCCTGGTCACCCAAAGTCCCCCAAATCCCCTTCAAATTCCTAAA
TCCATAACCCCATCTGTCCCCATGTGTCCCTTTGTCCCCAGTGCCTTC
CGGGTCTTCTCCATGGACCCCGACCTACAGCCGAACCCCGAACCTGTCTC
GGTCACCATCACGGTATGGGCCCTATAGGGCTGGGGCTGTGGGTGACCCT
GTGGGGTTTGGGTGACCCTACAAGGCTGTGTACCCCATGTACCCCCAGA
ACCGTTGGGTGCACGAGTGCAGGGAGGTGCAGCGGGTGGCCCTGGACACG
GTGCTGAGCGACAGCTGGTGTGCTGCCTGACATCGCCCTGTGAGTGGGGCT
ATAGGGGGCTACAGAGGGCTGTGGGGTGCAGAGGGGGCTATGGGGACTG
GGGACTATGGGGATTTGGGGCTACAGGGGCTGCAGGCGGGCTAGAGTAGT
GGGGGGGATTATAGGGTTACTGGGGCATTACAGTGGCCATAGAAGCTATA
GAGGGCTGTGGAGAACTATAGGATACCTTAGGGGCCATAGGGGTCTACAG
GGGTATAGGTGAGCATGGGGAAACATAAGGGCCATAGCGACTCCGGAGG
GCTGTAGCACACCATAGGGGGCCATAAGGGCCCTGGAGGGCTCTAGAGGAC
CACAGAGGTGTATGGGAGGGGCTATAGGGGACTATAGGGTATAT

FIGURE 10

SUITE 59

97/110

E52FOR.txt

ACATGGGAACACATGAGGACAGGGAGAACTGCAGGGACACAGGGACACT
TGGGGGATAGGGGGATGGTAGTGATGCATGGGGGGGGGCACATGGGGATG
TGTTGGGGCACACTGGGATGTGTGGGGATATGGGGACACATGGGGGAATAT
GGGGATGAGTGGGGACATATGGTTATTATAGGGATGTATGGAGACATTGG
GACACATGCAGAGGAGGGGACAAATGGGGACACACTGGGGGACAGATAGG
GACATGGGGACACCCAGGGAGGGACACCCCAAGTTCCCCCTTACCGGCGG
CAGTGATGGTTCCTTCTGTGCCCATCCCCCTGCAGCAGCGCAGTGACA
CCGTACTGCGGGGTCCCCACCGCCGCCACCCACCACTGCCCCCGCGGT
TGGGGGGCTGCGGGCGTCTGGGGTGCAGAGGGCGGCTCCATGGGTGAGAGC
CGGTCTGGGGGTTCGTGGGGTTCAGTTCGCAGCTGGGGGGAGTCCGGGGG
GGGACCCGAGTGGGGTCAGAGTCCCCAGGGGTCTGCGAGGGAGAGAGG
AGTGAGAGGGATGAAGGGTCTGAGGGCATGGGGTTGGGAGGGGTGTGGG
GCGTAATGGGGTCATTTTGGGGTTAATGGGGACACTGGGGACAGTTTGGG
AGCTATTGGGGCTAATGGGGTCTCTGGGGGACATGGAGGGGACATTGGGG
ACATTTGGGGTGTAAT

FIGURE 10
SUITE 60

987110
E52REV.txt

TGGCTGATGGGCTGTGTCCTATGAGCGCAAAACACCACAATGGGCAGAAA
AACCTTCCTCCAGAGGACCAACCCCATCTCTATGGCTTCTTGCACCTGG
CCTTGCCCAAAATTGGGTTATTTTGGAGAAAAAATGGGCCATTTCTCTG
CTGGTTGTCCAAGCAGCAAGAGATGCTGGCATGAGTCTCACCAAGCCAAG
AGGTCTGTGGGACCAAGAGAACTCTTTTCTCTCCATTAATGATGAGTAA
CTCCACCTTTGGGCACTCTTAAGGTGAAAATCCTCAAATCTGCAATTTT
GAAGGCGCAGCTCCACATTTCTCATCCCTTTGTTCTGTCCATGGCAGT
GCAGGCATTCCAGCCCCATCCCCAGCCCTGTGCTCAGTGTCCCTTCGACT
GGATTGGATTGAGAGGAAAATGCTACTACTTTTTCAGAGGATGAGAGCAAT
TGGACGAGCAGCCAGAACAACTGCTCTGCTCTTGGTGCTTCCTGGCTGT
GTTTGACAGCGCTGAGGACTTGGTGAGGGGGACACAAAAGAGCCACCAAT
GTATTTTGTCCGCTTGAGGGCCCCCTTGGCTGCTCTTTTCAGTGTTCCTTT
CTGATTTTGGGGTGAGGAGGTGGATAATGGTTGTCTGAGGGTAGGTTGG
GTCTACTCCTCAAATTTCTCAAGGGATTTAAGGGAAAAAAGATGTTT
TTTCTATGAAGTAACCAGCTGGCTTAGAGACTGTGAGCTTTGGTGATGG
ATTGGGCAGTTTCAAGCACTGAGATTATGGTTGAAAGGGTTCTGCAGGC
AGTGGCATGCAGGAAATGTCCAGAGCCCCATGATCTGTTCCCTCTCCTC
TTTTCCAGAGCTTCACAATGAGACACAAAGGCAGCTCCCCCACTGGGTT
GGCCTCTCCCGGAAGGCAAAGAGCATCCATGGGAATGGGTGAACCGCTC
TCCTTTGTCTCACCTGTGAGTTCCCATCCTTGTCTTGGAGGCTGCAGCTT
CTCCAGCCCCAAAATGTGGATTTCTGGACCTCGGGAGCATTCTGGAGGT
GGCTTATGGGGTGAGGAGATGTGGGGAAGGCACTTCGCACCGCTTTGGGT
CATAGAAGTTCAATGAGAGGCAGAAGTGGCGCAGGAAAAAGAGATTCCTA
TTTAATCAATTATTTTGTCTGTTTGATTTCAACCACTGTGATTTCTCTTC
CCCCCCCCCAMAACCTGGGGTCTGCCTGTCCTGTCTGTCTGTCCATCCA
GGTTCCAGGTGCAAGGCGATGGTCTCTGTGCATACCTGGGGGATGCCGGG
CTCAGCTCCTCCCACTGCAGCAGCGGAGGAATTGGGTTTGCACCAAACC
CGCGTTGCAAAAACCGAGGAAGAACTTCTGCATCAGCACCTGAGCGGCTC
CCGGACCCGAACACGCGATGCAAGAGGAGGAACCCAAAGCAAAAGAGCTC
CGCTTTCAGCTGTGCTCAGTAGCAACAGGAGGGCGGTGCGCTCCTCCAGC
CCAGGTCCGACAGTGCCGCTATGGGGCTGCGCGGACCGAAGCAAATCCC
AGGCGGAGCTTCGGCTCCAAATTACATTTTTTTGACCGTCTGACTCCTA
ATGACCGCTAAAAATCCCAATTTTGGGGGCTATCCGTGCGCTGCTTGCAAC
GACCTTCACCCCTGCGCGATGCAGCAGCAGGTTTGGGGGGCGGACGGTGG
GAAAATATCCATTTTTCACCGGTTTTCTCAAAGGGAATACTGGGAAA
GCAATCAGCCCAAAGGACCCTGAAATCGATGAATAAATCGGCAAATTATT
TATGTTTTCGTGTTTTCCCTTCTGTGTCACTGCAGTGCCTTCTCCATGAAT
TCACTTTTAACGGTGTTTTGTACAGGAAACACTTCTTCGACTCTCTCCA
CCTCTCTATATATTCAACAGACCAATTCTTCTGGTGATTTTATGCAAA
AACAAAAGAGTATATTGGTTAAAGAACCCAAACCACCTTCTTGTACTGA
AGGGAATAGAAGAGCACAGACCGCCCGCTCCCTCCCTGCTGCCGCACA
ACAGACGGTCCCCGAGGATGTGCAGACAACGCGACGCGCTCTGA

FIGURE 10

SUIITE 61

WO 99/27132

PCT/FR98/02501

99/110

E6G2N15.txt

TAGNAACTAGNGGATCCCCCGGGCTGCAGCTATGGGGGAGTGGGTGCACT
CCTTGCCCATGGCTTTGGGTCCCGTTACTCTGGAGGAATTTCCACAGCTG
CCCCAGGAATCTTGTACATAAAAGTGCACAGATCGATCAGAGATGTCATG
TTCCTGACAGAAGAAATCCTGTCTCTTCTGATGTTCTCTGTGAAGAGCAT
TGCCACGAGGGAGCTACCAGCAGGGCAAGCAGAGAAATTGAAGAAAACGA
AAGATGGGTGAGGTACGGGATTGGGCAGGTTTCACTTTCTTTAGCAATG
AGACGTGTCAAGCTGGCAGCTTCCCTGGGAGCCTCTCTGGTGTGGATCTC
CGGTGGCCCTAAACCTGGTTCAGGCACTGATCAAGGAGACATTACCCGTC
TTGGTTCATCTCGGCTCACGG

FIGURE 10

SUITE 62

100/110
F12FOR.txt

CGATGGTCCTCCAATGACCTCCATGGTCATCCAGTGCTCATCCCGCGGTA
TGGCCATGGTAACCCCATGTTACCCCTGTGGTCTCACCCCAATGATGCCG
TGTTTACCTTTTCGTTACCCCTATTCTCATCCCATATCCCCCTTTCTGTC
CCTCTGCCCCCTTCATGATCCCCCTCATGGTTAACAGACGTTTCCCTCTGCG
ATCAGGTCATGTTCAGCACAAATTCCTCCAGGGTTCCTTTATAGTGACC
TCACCATTACCCAATCATGTCCCCGGTGTCCCTGAAGGGGCCAGATTTC
CTCAGTGGGACCCAGATGTCTTCAGTGGGGCGGGACCTGGCCATTCCCAA
TGTCATCCAGGTGTCCATATGGCATGGGACACAGATGTGCACATGGGATG
GGACCCAGGTGTCCCCACTGTTCATCCAGATGCCTCCATGGGTGGGAAAT
GACCATCCTCGATGTCACCCAGATGCCACATGTGATGGGACGTGGCCAT
CCTTCATGGCATCCCGATGTCCAGCTTGGGATGGGATCCCAATGTCACCC
AATGCAATCGCAGTGTACCCAGATGTCCACAAGGGATGGCACCCAGATG
TCCCCAGGTGCCACTCATCTGCCTCACCAACCCAGGACTTCCTCCCACTG
CTCCCCACTGCTCCCAGTTTGCCCCCATTTCTCCC

FIGURE 10

SUITE 63

101/110

G2M13.txt

GATCTTCAGTGATTTTCAGTGGTCTTTGGTGGTCTTCAGTGCTCTTCGTT
GGTCTTTGACAAAGATGCAGAGGAGCACCGCTCCCAGACGGACCCCCCGG
GGACCCCATTTGTGCGCCATCCCACTGGGACATGCAGCCATTGACCACAG
CCCTCCGGCTGCGACCACTGATTCTTATCCAAAGTCCACTCTTT
GCACACTTACCTCCAATTTAGTGATAAGGATGTGGCGTGGGACCGTCCCA
ATGGCCGCACACAAGTCCAGGTAGATGATATGGGATGACCATGAAGGGAT
CACAGAGAGGAACACGGGGTGACCACGAGGAGCAACGAAGGAAACGCTGA
GTGACCACGGGCAGAAAATGGTGTGACCATTAGGGGACAACGAGAGGGAA
CAGAAAGTAGTAAGGAGTGAGAATGGGGTGACAAAGAGGTGACCATGGCAT
AACTTTGATAAGACCATTGGGTGACCGCAGGGTGATGGCCATACCATGGG
GTGAGCACTGGATGACCATTGGAGGTCATTGGAGGACCATCGGGTGGGACG
AGGGCCGTGGGGACACCCGTGGGGCGGTGGGACGGGGGACAGTGTGAGA
AGGAGCCCCGCGGCGCAGAACTCTGCCTGGAGACGGGTGACGCGCCCGG
CGCCGCGCGCGCTCATTGGCCCTCCCCGCGCGCGCGCGGCTCGCGGCTG
GCGCGGGGTGCGGGGTCCCCCATCGTCCGGCGGCAGCAGCCATGGGGAGC
GGGCGCGTCCCGGCGCGGGGGCCGTGCTGGTGGCACTGCTGGCGCTGGG
AGCCCGGCGCGCGCGCGGCACGCGGCCCTCGGGTGAGCTCGGAGCCGCGG
CGCGGGGACGGCGCTGCGTCCCCCGGAGAAACCCCGGAGCCCTTCTG
GCCGTGCGCAGCGCTCGGGGCTGCGGGGGGACGGAGGGCGGGGGGGGGCG
GCGGAGCCGTGGGGGGCAGCGGGGCCGGGAGGGGGCGGGGGGTGTGGCG
GGGGCGCGTGTGTGCCCTGACCGTGCCCTCTGCGCGCAGCGTTCTTTCTT
CTGCGGTGCCATATCCGAGTGCCACTACCTGAACGGCACCAGCGGGTGA
GGTATCTGCAAAGGTACATCTACAACCGGCAGCAGTTCACGCACTTCGAC
AGCGACGTGGGGAAATTTGTGGCCGATTACCGCTGGGTGAGCCGCAAGC
TGAATACTGGAACAGCAACGCCGAGCTTCTGGAGAACC GAATGAATGAAG
TGGACAGGTTCTGCCGGCACAACTACGGGGGTGTGGAGTCTTCACGGTG
CAGAGGAGCGGTGAGTGCCGCGGGGGCGCAGCGCGGACGGACGGGCAGGCG
CCGCGCTCTGGCGGTGCGTCCGCAGCGCTCCCCCGTGCCCCGCACTGGA
GCCCCAAGGTGAGGGTCTCGGCGCTGCAGTCGGGCTCCCTGCCCGAAACCG
ACCGTCTGGCGTGCTACGTGACGGGCTTCTACCCGCGGAGATCGAGGTG
AAGTGGTTCTTGAACGGGCGGGAGGAGACGGAGCGCGTGGTGTCCACGGA
CGTGATGCAGAACGGGGACTGGACGTACCAGGTGCTGGTGGTGTGGAGA
CCGTCCCCGCGCGCGGGGACAGCTACGTGTGCCGGGTGGAGCACGCCAGC
CTGCGGCAGCCATCAGCCAGGCGTGGGGTAAGGCCCGCGGGCCCTGCCC
CGCCGCGGGGGGAGCGGGAGCGCGGCCCGCGCTGAGCCGCGCCCTTC
GTCCCCGACAGCCGCGCGGACGCGGGCAGGAGCAAGCTGCTGACGGG
CGTGGGGGGCTTCTGCTGGGGCTCGTCTTCTGCGGCTGGGGCTCTTCG
TGTTCCTGCGCGGTGAGAAAGGTGAGCGCTGGGGAGGGGGGCTGCGCCG
GGGGGGTGGGAGCGGGGGG

FIGURE 10

SUIITE 64

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H421.txt

GCTCTAAGAACTAGTGGATCCCCCGGGCTGCAGGATTACCACTGTCCCAA
CTGTTTATGCGCAATCCAAGCCCTGCAAATGTACAAATATATTAAGTGGTT
TCCTTAATAGACATCTTTATATCTCTCACCATCATTTAACGTTAACCTT
ACTCTGCTTTCTTCTGTGAACAGAAAACAAAATCGGAAGCCTCATATACA
GGTGTTCAGAGGAAAATAGTAAGTGGTGATGAACTTGGAGAAGTTGTGA
AGTGAAATATGGGAGCTACTGCCTCTGGAGGGAGGAAAATAAGGAACCAA
TGAAAGATGCCAAGGTGAAGCAAATGAAGGACCAGCTGTTGTGGCTAGA
GCATACATCCCAAGTATTGCTAAAATGCCTTCTCAAAGCAAGTTGACTCG
GGATATGAAACAGAAATATCCAAGAGTTTGAGCGTATTCTTAGTGAAAGTT
CTCAAGATGCTGACCTTCCACCACAGTAAGTTCTCTCCAGTTTGGGTTTA
ATCATTATTTGTAAGTAAAGTTTAGTTCTTACTGGAAAAGATTTTGTG
GATTTCTAGTCACATGAATCTCTCCTAGTTTGCCTTCAGTTTGCCGGACA
TCCCGTTTCTAGTGGTTTTACTTGCTT

FIGURE 10

SUITE 65

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H4212.txt

TAACCATGAGTGATAAACTGCGGCCAACTTACTTCTGACAACGATCGGA
 GGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAAC
 TCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACG
 AGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAATA
 TTAAGTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTG
 GATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG
 CTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGC
 GGTATCATTGCAGCACTGGGGC

FIGURE 10

SUITE 66

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H424.txt

TCCCTAGTAACGGCCGCCAGTGTGCTGGAATTCGGCTTAGCGTGGTTCGCG
GCCGAGGTACATACCCTGCCCAGTGATGTCTCCAAGGTTGATTTAAGC
AACCAGCTCCTCCCTGCCACGGCTCCAGGCTCCACATGCCTGGGTTAAGG
CTGGGTTTGTTTTTTGAGACAGTGTCTTAACATATGGAGCGCTGACTGTTT
TGGAACCTCGCTCTGTAGACCAGTCTGGCCTTGAACCTCAGTGATCCCCCTG
ACTCTGTCTCCAGAATGTGGATTCTCCCA

FIGURE 10

SUITE 67

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H4REV.txt

GGATTCTGACACCCCTCCTCCCCACCCCAAGGTGTTCCAGCGCCGCA
TGGATGGGGGCACGACTTCTGGAGGGGGTGGGAGGAGTACGTCCATGGC
TTCGGGAACGTTTCTGGGGAGTTCTGGCTGGGTGAGGACCCAAAACCTTG
GGAAGATTGAGGTCTGGGGTGGGGGGGGGAACACCCAGGGCGGAGAGGG
CTGATGGCTGCAGGACGTGGAGTGGGATCCCTGACGGGGGTGTGGGGTGG
GGGGTGTGGGGCAGGGGCCCCAGGTGGGTGTGTAGGGTGGGGATGATGAC
GATGGCTGTGGGATGTGGCGCAGGGAATGCGGCGCTGCACACACTGACAG
CTTCCGGGGCCACGGAGCTGCGTGTGGACCTCTGGACGCCGTCAGACAGC
GCCTTCGCCCCGCTATCGGGATTTGCGCGTCAGTGGTCTTGAGGACAATTT
CCGCTTCACCTCGGGGCCCTACAGTGGCACAGCTGGTGTGTGTGGGGCAG
TGGGAGCTCCTGGGGGATATTAGGGTTAACCTTGACCCATGAGGGGGGCT
TTTGGGGATACCCAGATCAGGGGGGGGGGAATCCTGGGGAGAGTAGGGG
ATGGTCCCTTTGCCACAGTGAGGGGGCCTTGCCTTGCAGAGGTCTTTAA
GATCGTTGACCTGTTGGGATCTCTTGGGGATCTCCAGACTGCAGGGAGCC
CCGGGGGTCTTGGGGGGCTCTGCCCCACAGGGTGGTCTCTGTGAGGGTG
TGGGGGTACCTGGGGGGTCTGCGGCTCATCCTTGGGGCTCTGAATGCTAT
GTGGGTGTCTTGAAGGCTCTCTTTAGGGGTCCCCATAACCTTGCTGTGG
GTCCCACAGGGGATGCACTGTCTTACCATGCTGGGAGCCCTTCTCCACG
CGGGACACGACCCCCGAGGCCGCCCTCGGCCCTGCGCCGTGCGCTACAC
CGGAGCCTGGTGGTACCGCAACTGCCACTACGCCAACCTCAATGGGCGCT
ATGGGGTGCCCTACGACCACAGGCATGGCTATGGGGGTGTAAAGGGGT
CTGTGGGGATTGTAAAGGGGTCTATGGGGGTATAAAATCAACCCAATGGG
ACAGGAGGGGGTCACCATGAGGCCATGGGGGTTTGTGGGGTAAATGTGG
AGGGCTACCCCCCCCCCAAGGTCCTTTTAGCCCCATGTCTCTCTGTATG
AATATGGAGCCCTACAGGAGCTGTGGAAGCTGGAACACAAGCTGGAACAG
GGAGGGGATACTTTGGGCCCCCTGTAAAGCCTATATGTGTCTATAGGGT
CACTGTAGGTTGTTTAAAGGCATGACCAAGTCCCCCTTCCTTTCTGCAGG
GCATCAACTGGTACCCCTGGAAGGGCTTTGAGTACTCCATCCCCTTCACA
GAGATGAAGCTGCGACCGCAGCGTGAAGTGAAGCACTAGAAAGGTCTGTGG
GTCGCACTGGAGCCTTTATGGGGTCAATAAAGCTGCGAGTAGCCAGTGCT
GACCCATGTATCCACACACTGGGCTCAGGAGCTATGGGGGTGGGCAGGG
CGTGAGGCGCACGCGGAACGGGGCACAGCGCAGCACGGTGCCAGCAGTGA
CCCCTAAGTGGGGCAGAGCCCCATCAGACGGTGGCTCCAGGCGGAATCGC
TGTAGGATGTGCCCCAAAACACAAAGAGCTCTGCCCCGAGCCAGCGCCTC
CCCCACACAGAGCGTGCCCCACAACCAAGGGCAGCAGCGCTCGCCATG
GAGCCCCCGGCTGCAGGAACCGCTCTGTGGGGCAGAACAGAGATCAGAGT
GGGTGTAGGGGGAGGAACCCAGCCTGGGGTTCAAAGCCCACATCTATGGG
GTGGACCCACACATAACGGGCAGGAACCTCATCAGGACGGTCCCAAATCTT
GGGGTCTGTTGGTGCAGCAAAGAGGTTTGGGATAACGATGGATCCCGCAG
GCACTGGGATTCCCGCAATGCTGGGAAGGGACAGAATGCTGATAGGATGG
ACTGGGAGAGCCTACAGAGGCCAAGTGGGACATACTGGGACCTGCTGAGC
TATCCTAGAGCTTACTGGGTGCTTGTAGTGTCTACTGGGACCGACCTAC
TGGTAGGTCATGCTGGTCTGTAGTGGTCCACACTATTACAGACTGGTCT
ACAATGGTTTCATTCTAGTGCAAAATACTGACACGAGTGGTGCACGGTTC
TGCTCGCAGACATGTGGCCCCGCACTGGTTGGTACTGATCCCCACTGGTCT
GTATGGCCCCATAACAGCCCGTACTGGTGTACTGGCTGTACCTGGAGTG
GCGCCGGGCACAGTGGGGCAGCGGAGGGGCACGGGGGGTGCAGGCGGA
GGGTCTCGGTGACAGTGGCACGGAGCAGTGGCAGTGGCCCCATATCCCCT
GGCTTTGGGGTCCCCCTGGGGCCAGCACCTGGCGCAGCTCTGCACGTAC
CTGGTCTGCACCTGGGACAGGGGACACGTGTCAAAGCACGTCACCAAGT
GCCACATCGGGTCACTTGTGGGGTGGCCCTCCCCTGCACGGGGACACAGG
CAGCAGCGTGACACGGAAGTGACATGAGCGTGACATTTTGGCACTGGCCA
CAGTGACGGGGACACAGGGGCATTATGCACACAGGGTTATGGACATGGA
TGTGACATGCATATGGGGAAGTGCACTGGAGCTATGGGAGGGGACAGCCA
GGACATGGGTGGGGAGGCGCAATGGGACCTGGGGAGAGGAGGAGTGTGGG

FIGURE 10

SUITE 68

TGTGACACAGATGTGATGTGGTGTACCTGGGGGTGGTGCAGCAGGAAGG
CCACAGCCCATAGCAGAGCCACTGCCGTGCTTTTCGGTGCCACCGATGAAG
AGATCCACGAGGGCCATGTGCAGGCGGTCCCCCCCCAGCGGCCCATAGG
GACAGTGGGGTCCCCCCCCAGCAGTGCTCCACGACTGTGTCCCTGGGGG
GAGACGCACAGCCCTGTGGGGACACACGTGTTACCCCTGGGGCCCTGTC
CCCCCCTGTACCTGTGTCCCCACGTTCACCTGGTGCCATCGGATCT
GGGACTCCACAAAGGCATCGCGGCGCTCCACCAGGCGCAGCAGCTCCCGC
AGCCCTGCGTTGGGCAGCACCTGTGGGGCACAGGGACCCCCCAGTGCT
CCACAGAGACCCCTGGACCCATAGGGACCCCATATTCCCTCCAGCCCC
ATATATAACCCCCCCCCAGGGCGATATAGCCCATCCTTAGTATAGACCC
TGCAGCCCCATATGGACCTATACCACCTCCTCTTATGACTATATCCCGCA
GCCCCACGCCGATCCTATATGCCCTGTAGGGCCCTGTAGGGCTCACCCCTT
AGTGAAGGCAGCACATCCAGTGCCCGCACACTGGCCCGGCCCCACACCTC
CAGCAGTTCACCACACAGCGCGTGAAGGAGCGCACCTCCGCCTCGGGGG
GCATCTGTGGGGCACAGGGCTTGGGGTCACCCAGAGAGACTCCTGAGTC
CCCCCAGAGACTCCTGAACCCAAAGAGGTACCGTGGTCATTTGGATCCCT
CTAGAGGTGACTGGGTTCACAAAGGGACACCTCAACACTTGTGTCCCTT
CAGGGGCACCTGGATATCTGGGACTCCAAGTGGCACCTGAGCATTGGGA
CCCACCCTCCTTGGACACCTGGGTACCCCAAGGACACCTGGGACCCCTT
CAAGTGGCACGTGGACATCTGAGCCCCCTGTAGTGGCACTTGAGTCCCC
TGCTCCCCCAGGTGACACCCAGACCCTGCAGCCCTCGATATCCCCACCA
GGTCCCCGAAGGCAAGGCGGCAGATGGTGCTGCAGGTGTGGAACGTGAAC
GCCTCAAAGAGGTCCACTGGGGCAGCCCCATAAGAGCTCAACTCCTGTGG
GGTGAGAAATGGGGTCACTGAGCGGGTGCGGGTGCCCCACAAGGGGGGT
GGGGTGAGTCAAGGGGACGGGCAGCACAGCCCTGGGGCTGATGGGGTCCA
CCTGGGGTTGGAGGGCCCTGTGTGGGGTGCTCACCTGGCACAGCGCCCA
GCCCTGCAGCTCCAGGAGGGGCTCCAGGTGCCTCACAGCTCGCGCCAGTG
CTCCCCGCTTGGCCCCGCTGCCGTGCGCACTCTGGGGATGCATCCCC
AGCGCCAGGTCTTCCCCCCCCCGGACACCAGGGACGCTGTGGGGTGACA
CCCATATCACCTGGCACCCATGTGACCTCCGAGAACCCCTCAGACAGCT
GTACGGATCCTTGGGGACACATCCAGAATCCCCCAGGCACCCACTGGGAT
CGCTCCAGCACCCATGGGGACTGTTAGAGATCTCCTCCCCCCCCAAAAAT
ACAACCAGACCCCTTCAGAGATCATGGGGACCCCCCAGTACCCCTCCA
GATACCAACAGTGAACCTATAGAGACCTCCTCCACCCAAAAGCCATGGG
GACCCCTCAGGCCCCCCCCCCCCAGACACCAATTAGTACCCCCAGAACCCT
TCAGAAACCTACAAGGACCCACCAGAACCCCTCAGATACCCATAGAGAT
CTTTACAGACCTCCTCCTGGGACCCTCCCCAGGAGCACAAATCCCAAAGA
ACCCCTTGAAGATTACAGGGACCCCTCTGACTCACCCCAAACCT
CATGGGGACCTCCCAACCCCTACAGCCCCCATACCCAGGTAACCTGTGG
GGGCGTCCACGAAGTCCCCCAGCGCCGTGCCAGTGCCTCACGGATGGC
TGCTGCAGAGCTCAGCACCACACCTCTGGGGGGGTGGGGGGGAGGGG
AAAAATGAGTGAGTTGGAAGGAAGGGACCCATGGGGACCCAAAAACC
AGGGAGAGGGAGAGGTGAGGGGTGCCAGAACGGAGTTGGGGGGGGGGG
GGGAGGGATCCCAAATTATTTTTTGGGGGGGGGGAGTAGAATGAGAGGAC
AAATTTGAAGGGGAGCAGAAGGAATTGGGGGACAGTATGTGGGGGTTCC
TCCATCCTCTCAATGGGTAATTCTGGGGAGCCTGTGAAGTTGAGGGTCT
AAAGGGGGAAGGCTCAAGGTCCCAAGGAGGAAGGGTTATGGGGAAAAGG
GGGTAAATGGTGGTCCCAAGGGGTATCAGGGGGATGGGGGGGGGGGGGT
CATGAAGGTGCCGCCCTACTCACACACCCCCCAAGCGCAGGCATAAG
GGGTCCCCGTAGGTCCGGGCAAGGATGTGGAGGTGCCGTGGCCCCCTGG
GTGCAGGAGGTGCAGGGCCCCCCCCACGGTGCTCCCCCGCCTGGCTG
ACCCCCCCAGATCAGAGCCAGGAGAAGTAGCAGAGAAGTATCGTCACC
GCCATTGTTCTGTGGGGTGGGGGGCCCCAGCTCTGCCCTATAACACCTT
ATGAGGAGGAGGTACCCCAAAGCTCCACCCCCCACATCCAAACCCCTC
CTACCAGAAGAGGGGCATTGGGTTCACTCCCCTAAAATTATTGTGTGCC

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUITE 69

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H4REV.txt

ACCCCCCTCTTCAAGTCATTATAAACTTTACAGGGGTGTCCTCATAAAAA
TACAGGAGTGTGTCCCCCACAAAGTGCTCCAGAACCATCGGGTGCCCA
TCCCACAAGAAAATCTCTCAAACCTCCATTGTGTGCCCCCAACCAACAA
AGATTCTCTCAAACCTCCCCCCCCCGCCCTCTACCCATATATCCTCCCAAGC
GCTCCCCACCCCTCCGCACACCACCTCCCCAAATCCTCCCCCATTACCAT
AATCCCCCCCCACCCACAGCAGCAGAACCCCATCACCGCTCTGTGCGTCTGT
GTGTGTGAGTAGGGGACGGGGTGTTTATTGAGGGGAGGGGGAGGGGGGA
GAGCGCTCAGAACCCCTCCCCCTGCAGCCCCCGCAGGCGCCGTGCCAGCT
GCAGGTCTTTGGGGTACAGTGTGACGCGGCGCGCATGCAGCGAGCACAGG
TAGGCGTCTCTCCAGCAGGTGCACCAGGAATGCCTCCGCCGCCTGTGGGAC
CCCGCGTGGGCGTCCCCACAAAGCAGGGGGGGAGTCAATTCCCACCCCC
AGGCCACCCCAAAATGCCAATCCTCCAAAATAATCCTGGAACAACCCC
AAAAAAACCCCTACCCCCAACCCCTCCCCAAAACCATAACCTCAATAA
CTCCACACCTCAAAAACCTCCAACCCCTCAAAAACAACCCCAACCCCGA
AACACCTCACCCCAAGACCCCTTCCCAAGCCCCAAGAGACCCCAAGG
CACAAGGGGTACCCCAAAATCCACTTCCCCCTTCCCCCAAAAAGCCCTT
TTGGGCACTAGAGAGCTCCCCAGCACCCACCCAAAGGGTCCCCACGGTAT
GGGGTACCCTAAAACACCCCCCAACCCCAAAACCACGGGAACTTCCAAAAC
AAAGCTACCCCTTCCCCCCCCCCCCCAAAAAATAAACCCATAGGGCCCC
CCACCTCCTGTAGGGCCAATAGGGCCATAGCCTGCCACCTGTAGTCCACG
CCCCGTGTGAAGAGCAAGCAGATCTCCCGCACCTGGGGGGGGACAGGGGG
GCATGGGGACACTGGGGGGACATGGGGGGGGGGGGGGAGGGGGGGGGGG
GGGAGGGGCATGAGGACATTGAGGAGAGGGAACACGAGGGTGGCACTGCA
TCATGGGAGGTGACGAGGGGTGGGGGGGGCTCAAGGACATGGAGGGGGA
CACTCA

FIGURE 10

SUIITE 70

WO 99/27132

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H6FOR.txt

TTGCTGCCTGCAGGTCGATCTAGTGGATCCGCCGCGACAGCGAACAGGCC
AGCCAGCTGGTGCAGTATCTTTCCACTTTTTTCCGCAAAAACCTAAAGCG
GCCTTCGGAGTTTGTACTCTCGCCGACGAAATTGAACATGTGAATGCTT
ATCTGCAAATTGAAAAGGCGCGCTTCCAGTCGCGGTTGCAGGTCAACATT
GCTATTCGCAAGAATTATCCCAGCAGCAATTGCCCCGCGTTTACCCTGCA
ACCC

FIGURE 10

SUITE 71

Conti205.txt

FIGURE 10

SUITE 72

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Conti205.txt

CATCCCACCCCTACAAGTTCAACCTTTACGGGGTGTGGGGGCAGACACGT
CTGGGCCCCATCTCCACTGACACCATCACAGGTGAGGGCCCCCTGCCTGCT
GCTGTGCTCTGGGCCTTGTGCTTGGCACGTGGCAGGAGCTGTGCGATGGG
CTGTGCTGGTGGCGGGGATCTGACTGGAAATGGAAACGTTCTGTGGCAAA
GAGTGGGAATGTAGGAAGGGGGTGGGAGCATGCAGGGTTGGTGGAGCAGG
GGGTAGTGATCAGTGGTGAGGATTTGGTTTCTTGGTCTGAAATATGGATG
GAAGCTTTGTTGGGAGAGTGAATGACTTTTCAGTGAGGACAGGTGGATGC
TTGGGTGAATGCTTGGTAAGTTGTTGAACGCCTGGATAGTTGGATGGGTG
GACATGAACTTTGTATTACAGCTGCAGCTCCAGCACAGAAGGAACCGCCA
TCCCAACCACGCCTGGGTGAGCTGACGGCCTCCACGTGAGCCCCGACTC
CGTCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGG
TGAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACGGT
GGGTTGCGCACAGTGACCGTGCCCGGGCTGTGCGCGTCCCGCCGCTACAA
GTTCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCA
CTGATGCTGTACAGGTGAGCATGCTGTTGTGCTGCATCCATGTCTTTTG
GCTGACGGTTGTGTTGGCATATGGTAGGAACCTTTGAGGCCACTCCTGG
TTACTGTGGTCTTAATAGAGAGGGAAGTTCTTTCCTGTTCTTGACGTGGG
TAGCCTGGAGAGATGGGAGTATGGAAGATGAGAGGAAGAACGGAATAAGG
AATGATTGATAATTATTGCAGAACGGATGGAAGGGAGGATGGATGGGCGG
TGCATGGGTACATTGGTGCTTATAGCAGAGCTGGACGGCTGGTTGTACGT
TGGTTTGGTTGTTGAAGAGATGAAGAGTTGGATGGGCGTGTGCTTTTCACT
GTGAATTCCTCCCCCTGTCTTGCAGCTCCGGCACAGAAGGAACCACTTC
CCAGCCACTCTTGGGTGAGCTGACAGCGTCCACGTGCGCCCCGACTCCG
TCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGGTG
CAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACGGTGG
GTTGCGCACAGTGACCGTGCCCGGGCTGTGCGCGTCCCGCCGCTACAAGT
TCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCACT
GATGCTGTACAGGTGAGGGCAGGAATTGGCACCTGGTGGGCTCTGGGTT
TGCAGCAGGTAGAAATGTAAACGTGGCCTGCGCTGGGGATCTTGTTTTCC
CCTGGCAATGGGAACAGCTGTTGGGTGCCTTTTTTGGGAAGGATCCCTTA
ATCGCAGCATGAAGTATGAATGGACCAATTGGGTGTGGGTGGAGTGATGG
CTGTTGAGATGAGTTGGTGGCTGCTTGAGTAATTGTCTGTTGGAATGGAT
GGACAGATATGTGAAGGAGTGAAGGATGGATAAAGTAATTTAGGAATCG
GTGGATGAAGAATGGGTAGGTAGACCCTTGGTGAAGTGGTAGAATGGAAG
GATTTATGAACAGATATGAGTTAATTCTTGCATCGAAGTAGGTGTAAGTG
TCTATTAGCCTGTTGCACTGAACATGCAGTTGCATAGACAAATGAGTGGG
GAGAAGTACGGAGTAAATCCCTGCATGAATGGTAGGACAGAAACCTGAAT
GCCTGGATGCTGGCAGTGTGAAGAATGGCACTTGGGATAGATGGTTGAG
TATGGGGTAGATTAAAAGATGGATGGAAAAGAGGAACAGAGAGAGGGTGA
TTGGATGAATGGATGGATGGTTGGATGTGACTGATTGACAGGTACCAAGC
TTTTTTCCTGCACTGTGCCTTCTGTGCTGCAGGACTATGGTCATAGCTGT
TTCCTGTGTGAATTTGTTATCCGCTCACAAATCCACACAACATCGA

FIGURE 10

SUTTE 73

INTERNATIONAL SEARCH REPORT

International Application No

PCT/FR 98/02501

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>GUILLEMOT F. ET AL.: "Physical linkage of a guanine nucleotide-binding protein-related gene to the chicken major histocompatibility complex" PROC. NATL. ACAD. SCI. USA, vol. 86, - June 1989 pages 4594-4598, XP002074404 See the whole document , esp. discussion --- -/--</p>	1

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

20 April 1999

Date of mailing of the international search report

03/05/1999

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Authorized officer

Müller, F

INTERNATIONAL SEARCH REPORT

International Application No

PCT/FR 98/02501

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>GUILLEMOT F. ET AL.,: "A molecular map of the chicken major histocompatibility complex: the class II beta genes are closely linked to the class I genes and the nucleolar organizer"</p> <p>THE EMBO JOURNAL, vol. 7, no. 9, - 1988 pages 2775-2785, XP002074405</p> <p>See the whole document , esp. figure 1 et page 2783, 2. colonne</p>	1
Y	<p>MILLER M. M. ET AL.,: "Regions of homology shared by Rftp-Y and major histocompatibility B complex genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 71-73, XP002074406</p> <p>see the whole document</p>	1-10
Y	<p>WAKENELL P. S. ET AL.,: "Association between the Rfp-Y haplotype and the incidence of Marek's disease in chicken"</p> <p>IMMUNOGENETICS, vol. 44, - 1996 pages 242-245, XP002074407</p> <p>see the whole document</p>	1-10
X	<p>BERNOT A. ET AL.,: "Linkage of a new member of the lectin supergene family to chicken MHC genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 221-229, XP002100550</p> <p>See the whole document , esp. p.221, col. 1; p.222 col.1</p>	7-10
X	<p>ZOOROB R. ET AL.,: "Chicken major histocompatibility complex class II B genes: analysis of interallelic and interlocus sequence variance"</p> <p>EUR. J. IMMUNOL., vol. 23, - 1993 pages 1139-1145, XP002074408</p> <p>see the whole document</p>	7-10
A	<p>VALLEJO R.L. ET AL.,: "Non-association between Rfp-Y major histocompatibility complex-like genes and susceptibility to Marek's disease virus induced tumours in 6.3x7.2 intercross chickens"</p> <p>ANIMAL GENETICS, vol. 28, - 5 October 1997 pages 331-337, XP002074409</p> <p>see the whole document</p>	

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/FR 98/02501

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KAUFMAN J. ET AL.,: "Different features of the MHC class I heterodimer have evolved at different rates"</p> <p>J. IMMUNOLOGY,</p> <p>vol. 148, - 1 March 1992 pages 1532-1546,</p> <p>XP002074410</p> <p>see the whole document</p> <p>-----</p>	

RAPPORT DE RECHERCHE INTERNATIONALE

Demande internationale No
PCT/FR 98/02501

A. CLASSEMENT DE L'OBJET DE LA DEMANDE
CIB 6 C12Q1/68

Selon la classification internationale des brevets (CIB) ou à la fois selon la classification nationale et la CIB

B. DOMAINES SUR LESQUELS LA RECHERCHE A PORTE

Documentation minimale consultée (système de classification suivi des symboles de classement)
CIB 6 C12Q

Documentation consultée autre que la documentation minimale dans la mesure où ces documents relèvent des domaines sur lesquels a porté la recherche

Base de données électronique consultée au cours de la recherche internationale (nom de la base de données, et si réalisable, termes de recherche utilisés)

C. DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	<p>GUILLEMOT F. ET AL.,: "Physical linkage of a guanine nucleotide-binding protein-related gene to the chicken major histocompatibility complex" PROC. NATL. ACAD. SCI. USA, vol. 86, - juin 1989 pages 4594-4598, XP002074404 le document en entier, esp. discussion ----- -/-</p>	1

☒ Voir la suite du cadre C pour la fin de la liste des documents

☐ Les documents de familles de brevets sont indiqués en annexe

* Catégories spéciales de documents cités:

- "A" document définissant l'état général de la technique, non considéré comme particulièrement pertinent
- "E" document antérieur, mais publié à la date de dépôt international ou après cette date
- "L" document pouvant jeter un doute sur une revendication de priorité ou cité pour déterminer la date de publication d'une autre citation ou pour une raison spéciale (telle qu'indiquée)
- "O" document se référant à une divulgation orale, à un usage, à une exposition ou tous autres moyens
- "P" document publié avant la date de dépôt international, mais postérieurement à la date de priorité revendiquée

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- "X" document particulièrement pertinent; l'invention revendiquée ne peut être considérée comme nouvelle ou comme impliquant une activité inventive par rapport au document considéré isolément
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RAPPORT DE RECHERCHE INTERNATIONALE

Demande internationale No

PCT/FR 98/02501

C.(suite) DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	<p>GUILLEMOT F. ET AL.,: "A molecular map of the chicken major histocompatibility complex: the class II beta genes are closely linked to the class I genes and the nucleolar organizer"</p> <p>THE EMBO JOURNAL, vol. 7, no. 9, - 1988 pages 2775-2785, XP002074405</p> <p>le document en entier, esp. figure 1 et page 2783, 2. colonne</p>	1
Y	<p>MILLER M. M. ET AL.,: "Regions of homology shared by Rftp-Y and major histocompatibility B complex genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 71-73, XP002074406</p> <p>voir le document en entier</p>	1-10
Y	<p>WAKENELL P. S. ET AL.,: "Association between the Rfp-Y haplotype and the incidence of Marek's disease in chicken"</p> <p>IMMUNOGENETICS, vol. 44, - 1996 pages 242-245, XP002074407</p> <p>voir le document en entier</p>	1-10
X	<p>BERNOT A. ET AL.,: "Linkage of a new member of the lectin supergene family to chicken MHC genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 221-229, XP002100550</p> <p>voir le doc. en entier, esp. p.221, col. 1; p.222 col.1</p>	7-10
X	<p>ZOOROB R. ET AL.,: "Chicken major histocompatibility complex class II B genes: analysis of interallelic and interlocus sequence variance"</p> <p>EUR. J. IMMUNOL., vol. 23, - 1993 pages 1139-1145, XP002074408</p> <p>voir le document en entier</p>	7-10
A	<p>VALLEJO R.L. ET AL.,: "Non-association between Rfp-Y major histocompatibility complex-like genes and susceptibility to Marek's disease virus induced tumours in 6.3x7.2 intercross chickens"</p> <p>ANIMAL GENETICS, vol. 28, - 5 octobre 1997 pages 331-337, XP002074409</p> <p>voir le document en entier</p>	

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Catégorie	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
A	<p>KAUFMAN J. ET AL.,: "Different features of the MHC class I heterodimer have evolved at different rates"</p> <p>J. IMMUNOLOGY, vol. 148, - 1 mars 1992 pages 1532-1546, XP002074410 voir le document en entier</p> <p>-----</p>	